#5

SEQUENCE LISTING

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<120> ENZYMES HAVING ALPHA AMYLASE ACTIVITY
AND METHODS OF USE THEREOF

<130> 09010-108001

<140> US 10/081,872
<141> 2002-02-21

<150> US 60/270,495
<151> 2001-02-21

<150> US 60/270,496
<151> 2001-02-21

<150> US 60/291,122
<151> 2001-05-14

<160> 321

<170> FastSEQ for Windows Version 4.0

<210> 1
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<212> DNA
<213> Artificial Sequence

<220>
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gccgggattt cggcgatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg 180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta 240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacaccgc ccacgcctat 300
ggcatgaagg taatagccga tatagtcatc aaccaccgcg ccggcggtga cctggagtgg 360
aacccttcg tgaacgacta tacctggacc gacttctcaa aggtcgcgtc gggtaaatac 420
acggccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt 480
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gtcaagggct acggagcgtg ggtcgtcaag gactggctgg actggtgggg aggctgggcc 660
gtcggggagt actgggacac aaacgttgat gcactgctca actgggccta ctcgagcgat 720
gcaaaagtct tcgacttccc gctctactac aagatggacg cggcctttga caacaagaac 780
attcccgcac tcgtcgaggc cctcaagaac gggggcacag tcgtcagccg cgacccgttt 840
aaggccgtaa ccttcgttgc aaaccacgac accgatataa tctggaacaa gtatccagcc 900

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tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga    1020
agcactgaca tcgtttacta cgacaacgac gagctgatat tcgtgagaaa cggctacgga    1080
agcaagccgg gactgataac atacatcaac ctcgcctcaa gcaaagccgg aaggtgggtt    1140
tacgttccga agttcgcagg ctcgtgcata cacgagtaca ccggcaatct cggcggctgg    1200
gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg    1260
gccaacggcc agtacggcta ctccgtctgg agctactgcg gtgttgggtg a             1311

<210> 2
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
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<400> 2
Met Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Leu Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Met Gly Gly Ile Trp Trp Asp Thr Ile Ala
            20                  25                  30
Gln Lys Ile Pro Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asp Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Asp
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
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Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Ala Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
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<210> 3
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<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 3

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gccgggattt cggcgatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacaccgc ccacgcctac     300
ggcatcaagg tcatcgcaga catagtaatc aaccaccgcg ccggaggaga ccttgagtgg     360
aaccccttcg tcaatgacta cacctggacg gacttctcga aggtcgcttc cggcaagtac     420
acggccaatt acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac     600
gtcaagggct atgctccctg ggtcgtcaag gactggctga actggtgggg aggctgggcg     660
gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt     720
gccaaggtct ttgacttcgc cctctactac aagatggatg aggcctttga caacaaaaac     780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc     840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtatccagcc     900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga    1020
agcactgaca tcgtttacta cgacaacgac gagctgatat tcgtgagaaa cggctacgga    1080
agcaagccgg gactgataac atacatcaac ctcgcctcaa gcgaagccgg aaggtgggtc    1140
tacgttccga agttcgcggg agcgtgcatc cacgagtaca ccggcaacct cggcggctgg    1200
gtggacaagt gggtggactc aagcgggtgg gtgtacctcg aggcccctgc ccacgacccg    1260
gccaacggct attacggcta ctccgtctgg agctattgcg gtgttgggtg a             1311
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<210> 4
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 4

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Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Leu Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Met Gly Gly Ile Trp Trp Asp Thr Ile Ala
            20                  25                  30
Gln Lys Ile Pro Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Ala Ser Ser Glu Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
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<210> 5
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

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gcgggaatat ccgccatttg gattcccccg gcaagcaagg gcatgggcgg cgcctattcg 180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta 240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacaccgc ccacgcctat 300
ggcatgaagg taatagccga tatagtcatc aaccaccgcg ccggcggtga cctggagtgg 360
aacccccttcg tgaacgacta tacctggacc gacttctcaa aggtcgcgtc gggtaaatac 420
acggccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt 480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc 540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac 600
gtcaagggct atgctccctg ggtcgtcaag gactggctga actggtgggg aggctgggcg 660
gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt 720
gccaaggtct ttgacttcgc cctctactac aagatggatg aggcctttga caacaaaaac 780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc 840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtaccttgct 900
tatgctttca tcctcaccta cgaaggccag cccgtcatat tctaccgcga ccacgaggag 960
tggctcaaca aggacaggtt gaacaacctc atatggatac acgaccacct cgcaggtgga 1020
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tatgtgccga agttcgcggg cgcgtgcatc cacgagtata ctggtaacct cggaggctgg 1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct 1260
gccaacgggc agtatggcta ctccgtgtgg agctactgcg gggtgggctg a 1311

<210> 6
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 6
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20 25 30
Ser Lys Ile Pro Glu Trp Tyr Glu Ala Gly Ile Ser Ala Ile Trp Ile
35 40 45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
50 55 60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65 70 75 80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
85 90 95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
100 105 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr

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        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Leu Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Val Ile Phe Tyr Arg Asp His Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Arg Leu Asn Asn Leu Ile Trp Ile His Asp His
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435

<210> 7
<211> 16
<212> PRT
<213> Environmental

<400> 7
Met Ala Leu Glu Glu Gly Gly Leu Ile Met Gln Ala Phe Tyr Trp Asp
 1               5                  10                  15

<210> 8
<211> 26
<212> PRT
<213> Bacterial

<400> 8
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Met Lys Pro Ala Lys Leu Leu Val Phe Val Leu Val Val Ser Ile Leu
 1               5                  10                  15
Ala Gly Leu Tyr Ala Gln Pro Ala Gly Ala
            20                  25

<210> 9
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

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gccgggattt cggcgatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacacggc ccatgcctac     300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat     420
actgccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac     600
gtcaagggct atgctccctg ggtcgtcaag gactggctga actggtgggg aggctgggcg     660
gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt     720
gccaaggtct ttgacttcgc cctctactac aagatggacg aggccttcga taacaacaac     780
attcccgccc tggtggacgc cctcagatac ggtcagacag tggtcagccg cgacccgttc     840
aaggctgtga cgtttgtagc caaccacgat accgatataa tctggaacaa gtatccagcc     900
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gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg    1260
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<210> 10
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 10
Met Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Leu Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Met Gly Gly Ile Trp Trp Asp Thr Ile Ala
            20                  25                  30
Gln Lys Ile Pro Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
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                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Asn Asn Ile Pro Ala Leu Val Asp Ala Leu Arg Tyr Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Ala Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Ala Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
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<210> 11
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 11
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gtccccatgg gaggaatctg gtgggacacg atagcccaga agatacccga ctgggcaagc 120

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gccgggattt cggcgatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacaccgc ccacgcctat     300
ggcatgaagg taatagccga tatagtcatc aaccaccgcg ccggcggtga cctggagtgg     360
aaccccttcg tgaacgacta tacctggacc gacttctcaa aggtcgcgtc gggtaaatac     420
acggccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
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caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac     600
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gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt     720
gccaaggtct ttgacttcgc cctctactac aagatggacg aggccttcga taacaacaac     780
attcccgccc tggtggacgc cctcagatac ggtcagacag tggtcagccg cgacccgttc     840
aaggctgtga cgtttgtagc caaccacgat accgatataa tctggaacaa gtatccagcc     900
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tggctcaaca aggatacgct caagaacctc atctggatac atgacaacct cgccggagga    1020
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tacgttccga agttcgcggg agcgtgcatc cacgagtaca ccggcaacct cggcggctgg    1200
gtggacaagt gggtggactc aagcgggtgg gtgtacctcg aggcccctgc ccacgacccg    1260
gccaacggct attacggcta ctccgtctgg agctactgcg gtgttggctg a             1311
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<210> 12
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 12

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Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Leu Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Met Gly Gly Ile Trp Trp Asp Thr Ile Ala
            20                  25                  30
Gln Lys Ile Pro Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
```

```
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Asn Asn Ile Pro Ala Leu Val Asp Ala Leu Arg Tyr Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Thr Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 13
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 13

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atggccaagt acctggagct cgaagagggc ggggtcataa tgcaggcgtt ctactgggac      60
gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat     120
gccggaatct ccgcaatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt atgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacacggc acatgcctac     300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat     420
actgccaact acctcgactt ccaccccaac gaggtcaagt gctgtgacga gggcacattt     480
ggaggcttcc cagacatagc ccacgagaag agctgggacc agcactggct ctgggcgagc     540
gatgagagct acgccgccta cctaaggagc atcggcgttg atgcctggcg cttcgactac     600
gtcaagggct acggagcgtg ggtcgtcaag gactggctgg actggtgggg aggctgggcc     660
gtcggggagt actgggacac aaacgttgat gcactgctca actgggccta ctcgagcgat     720
gcaaaagtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac     780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc     840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtatccagcc     900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga    1020
agcactgaca tagtctacta cgataacgat gaactcatct tcgtcaggaa cggctacggg    1080
```

```
gacaagccgg ggcttataac ctacatcaac ctaggctcga gcaaggccgg aaggtgggtt    1140
tatgtgccga agttcgcggg cgcgtgcatc cacgagtata ctggtaacct cggaggctgg    1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct    1260
gccaacgggc agtatggcta ctccgtgtgg agctactgcg gtgttggctg a             1311

<210> 14
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 14
Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe
145                 150                 155                 160
Gly Gly Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln His Trp
                165                 170                 175
Leu Trp Ala Ser Asp Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Val Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asp Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Asp
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
```

```
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 15
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 15

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atggccaagt actccgagct ggaagagggc gggctcataa tgcaggcctt ctactgggac      60
gtccccatgg gaggaatctg gtgggacacg atagcccaga agatacccga ctgggcaagc     120
gccgggattt cggcgatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacacggc ccatgcctac     300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat     420
actgccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac     600
gtcaagggct acggagcgtg ggtcgtcaag gactggctgg actggtgggg aggctgggcc     660
gtcggggagt actgggacac aaacgttgat gcactgctca actgggccta ctcgagcgat     720
gcaaaagtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac     780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc     840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tttggaacaa gtacccggcc     900
tacgccttca tcctcaccta cgagggccag ccgacgatat tctaccgcga ctacgaggag     960
tggctcaaca aggacaggct caagaacctc atctggatac acgaccacct tgccggtgga    1020
agcactgaca tcgtttacta cgacaacgac gagctgatat tcgtgagaaa cggctacgga    1080
agcaagccgg gactgataac atacatcaac ctcgcctcaa gcaaagccgg aaggtgggtt    1140
tatgtgccga agttcgcggg cgcgtgcatc cacgagtata ctggtaacct cggaggctgg    1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct    1260
gccaacgggc agtatggcta ctccgtgtgg agctattgcg gtgttgggtg a             1311
```

<210> 16
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 16

```
Met Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Leu Ile Met Gln Ala
 1               5                  10                  15
```

```
Phe Tyr Trp Asp Val Pro Met Gly Gly Ile Trp Trp Asp Thr Ile Ala
            20                  25                  30
Gln Lys Ile Pro Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asp Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Asp
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Arg Leu Lys Asn Leu Ile Trp Ile His Asp His
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Ala Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 17
<211> 1311

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 17
atggccaagt actccgagct ggaaggggge gggctcataa tgcaggcctt ctactgggac 60
gtccccatgg gaggaatctg gtgggacacg atagcccaga agatacccga ctgggcaagc 120
gccgggattt cggcgatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg 180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagga gggaacggta 240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacacggc ccatgcctac 300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg 360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat 420
actgccaact acctcgactt ccaccccaac gaggtcaagt gctgtgacga gggcacattt 480
ggaggcttcc cagacatagc ccacgagaag agctgggacc agcactggct ctgggcgagc 540
gatgagagct acgccgccta cctaaggagc atcggcgttg atgcctggcg cttcgactac 600
gtcaagggct acggagcgtg ggtcgtcaag gactggctgg actggtgggg aggctgggcc 660
gtcggggagt actgggacac aaacgttgat gcactgctca actgggccta ctcgagcgat 720
gcaaaagtct tcgacttccc gctctactac aagatggacg cggcctttga caacaagaac 780
attcccgcac tcgtcgaggc cctcaagaac gggggcacag tcgtcagccg cgacccgttt 840
aaggccgtaa ccttcgttgc aaaccacgac accgatataa tctggaacaa gtatccagcc 900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag 960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga 1020
agcacgagca tagtttacta cgacagcgac gagatgatct tcgtgaggaa cggctatgga 1080
agcaagcctg gccttataac ttacatcaac ctcggctcga gcaaggttgg aaggtgggtt 1140
tacgttccga agttcgcagg ctcgtgcata cacgagtaca ccggcaatct cggcggctgg 1200
gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg 1260
gccaacggcc agtacggcta ctccgtctgg agctactgcg gtgttgggtg a 1311

<210> 18
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 18
Met Ala Lys Tyr Ser Glu Leu Glu Gly Gly Gly Leu Ile Met Gln Ala
1 5 10 15
Phe Tyr Trp Asp Val Pro Met Gly Gly Ile Trp Trp Asp Thr Ile Ala
20 25 30
Gln Lys Ile Pro Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile
35 40 45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
50 55 60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Glu Gly Thr Val
65 70 75 80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
85 90 95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
100 105 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
115 120 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
130 135 140

```
Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe
145                 150                 155                 160
Gly Gly Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln His Trp
                165                 170                 175
Leu Trp Ala Ser Asp Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Val Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asp Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Asp
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 19
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 19

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atggccaagt acctggagct cgaagagggc gggctcataa tgcaggcctt ctactgggac      60
gtccccatgg gaggaatctg gtgggacacg atagcccaga agatacccga ctgggcaagc     120
gccgggattt cggcgatatg gattcctccc gcgagcaagg gtatgagcgg cggctattcg     180
atgggctacg acccctacga ttattttgac cttggtgagt actaccagaa gggaacggtg     240
gaaacgaggt tcggctcaaa gcaggagctc ataaacatga taaacacggc ccatgcctac     300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat     420
actgccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
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caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac 600
gtcaagggct atgctccctg ggtcgtcaag gactggctga actggtgggg gggctgggcg 660
gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt 720
gccaaggtct ttgacttcgc cctctactac aagatggatg aggcctttga caacaaaaac 780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc 840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tttggaacaa gtacccggcc 900
tacgccttca tcctcaccta cgagggccag ccgacgatat tctaccgcga ctacgaggag 960
tggctcaaca aggacaggct caagaacctc atctggatac acgaccacct cgccggtgga 1020
agcactgaca tcgtttacta cgacaacgac gagctgatat tcgtgagaaa cggctacgga 1080
agcaagccgg gactgataac atacatcaac ctcgcctcaa gcaaagccgg aaggtgggtt 1140
tatgtgccga agttcgcggg cgcgtgcatc cacgagcata ctggtaacct cggaggctgg 1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct 1260
gccaacgggc agtatggcta ctccgtgtgg agctactgcg gtgttggctg a 1311

<210> 20
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 20
Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Leu Ile Met Gln Ala
1 5 10 15
Phe Tyr Trp Asp Val Pro Met Gly Gly Ile Trp Trp Asp Thr Ile Ala
20 25 30
Gln Lys Ile Pro Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile
35 40 45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
50 55 60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65 70 75 80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
85 90 95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
100 105 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
115 120 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
130 135 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145 150 155 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
165 170 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
180 185 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
195 200 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
210 215 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225 230 235 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
245 250 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
260 265 270

```
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Arg Leu Lys Asn Leu Ile Trp Ile His Asp His
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Ala Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu His Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 21
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 21

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atggccaagt actccgagct ggaagagggc ggcgttataa tgcaggcctt ctactgggac      60
gtcccaggtg gaggaatctg gtgggacacc atcaggagca agataccgga gtggtacgag     120
gcgggaatat ccgccatttg gattcctccc gggagcaagg gtatgagcgg cggctattcg     180
atgggctacg acccctacga tgatttggac ctgggtgagt actaccagaa gggaacggtg     240
gaaacgaggt tcggctcaaa gcaggagctc ataaacatga taaacacggc ccatgcctac     300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat     420
actgccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggtata tctcaggagc atcggcatcg atgcctggcg cttcgactac     600
gtcaagggct acggagcgtg ggtcgtcaag gactggctgg actggtgggg aggctgggcc     660
gtcggggagt actgggacac aaacgttgat gcactgctca actgggccta ctcgagcgat     720
gcaaaagtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac     780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc     840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tttggaacaa gtacccggcc     900
tacgccttca tcctcaccta cgagggccag ccgacgatat tctaccgcga ctacgaggag     960
tggctcaaca aggacaggct caagaacctc atctggatac acgactacct cgccggtgga    1020
agcactgaca tcgtttacta cgacaacgac gagctgatat tcgtgagaaa cggctacgga    1080
agcaagccgg gactgataac atacatcaac ctcgcctcaa gcaaagccgg aaggtgggtt    1140
tatgtgccga agttcgcggg cgcgtgcatc cacgagtata ctggtaacct cggaggctgg    1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct    1260
gccaacgggc agtatggcta ctccgtgtgg agctattgcg gtgttggctg a             1311
```

<210> 22
<211> 436

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 22

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Met Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Ser Lys Ile Pro Glu Trp Tyr Glu Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Gly Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Asp Leu Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Val Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asp Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Asp
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Arg Leu Lys Asn Leu Ile Trp Ile His Asp Tyr
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Ala Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
```

```
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 23
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 23

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atggccaagt actccgagct ggaagagggc ggcgttatag tgcaggcctt ctactgggac      60
gtcccaggtg gaggaatctg gtgggacacc atcaggagca agataccgga gtggtacgag     120
gcgggaatat ccgccatttg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacacggc ccatgcctac     300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat     420
actgccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac     600
gtcaagggct acggagcgtg ggtcgtcaag gactggctgg actggtgggg aggctgggcc     660
gtcggggagt actgggacac aaacgttgat gcactgctca actgggccta ctcgagcgat     720
gcaaaagtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac     780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc     840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtatccagcc     900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga    1020
agcatgagca tagtttacta cgacagcgac gagatgatct tcgtgaggaa cggctatgga    1080
agcaagcctg gccttataac ttacatcaac ctcggctcga gcaaggttgg aaggtgggtc    1140
tacgttccga agttcgcggg agcgtgcatc cacgagtaca ccggcaacct cggcggctgg    1200
gtggacaagt gggtggactc aagcgggtgg gtgtacctcg aggcccctgc ccacgacccg    1260
gccaacggct attacggcta ctccgtctgg agctattgcg gtgttggctg a             1311
```

<210> 24
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 24

```
Met Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Val Ile Val Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Ser Lys Ile Pro Glu Trp Tyr Glu Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
```

65 70 75 80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
85 90 95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
100 105 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
115 120 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
130 135 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145 150 155 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
165 170 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
180 185 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
195 200 205
Val Lys Asp Trp Leu Asp Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
210 215 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Asp
225 230 235 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
245 250 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
260 265 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
275 280 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
290 295 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305 310 315 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
325 330 335
Leu Ala Gly Gly Ser Met Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
340 345 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
355 360 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
370 375 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385 390 395 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
405 410 415
Ala His Asp Pro Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr
420 425 430
Cys Gly Val Gly
435

<210> 25
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 25

```
atggccaagt acctggagct cgaagagggc gggctcataa tgcaggcctt ctactgggac      60
gtccccatgg gaggaatctg gtgggacacg atagcccaga agatacccga ctgggcaagc     120
gccgggattt cggcgatatg gattcctccc gcgagcaagg gtatgagcgg cggctattcg     180
atgggctacg acccctacga ttattttgac ctcggtgagt actaccagaa gggaacggtg     240
gaaacgaggt tcggctcaaa gcaggagctc ataaacatga taaacaccgc ccacgcctat     300
ggcatgaagg taatagccga tatagtcatc aaccaccgcg ccggcggtga cctggagtgg     360
aacccccttcg tgaacgacta tacctggacc gacttctcaa aggtcgcgtc gggtaaatac     420
acggccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac     600
gtcaagggct atgctccctg ggtcgtcaag gactggctga actggtgggg aggctgggcg     660
gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt     720
gccaaggtct ttgacttcgc cctctactac aagatggacg aggccttcga taacaacaac     780
attcccgccc tggtgggcgc cctcagatac ggtcagacag tggtcagccg cgacccgttc     840
aaggctgtga cgtttgtagc caaccacgat accgatataa tctggaacaa gtatccagcc     900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga    1020
agcaccgaca tagtctacta cgataacgat gaactcatct tcgtcaggca cggctacggg    1080
gacaagccgg ggcttataac ctacatcaac ctaggctcga gcaaggccgg aaggtgggtt    1140
tacgttccga agttcgcagg ctcgtgcata cacgagtaca ccggcaatct cggcggctgg    1200
gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg    1260
gccaacggcc agtacggcta ctccgtctgg agctattgcg gtgttgggtg a             1311
```

<210> 26
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 26

```
Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Leu Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Met Gly Gly Ile Trp Trp Asp Thr Ile Ala
            20                  25                  30
Gln Lys Ile Pro Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
```

```
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Asn Asn Ile Pro Ala Leu Val Gly Ala Leu Arg Tyr Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg His Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 27
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 27

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atggcaaagt attccgagct cgaagagggc ggcgttataa tgcaggcctt ctactgggac      60
gtcccaggtg gaggaatctg gtgggacacc atcaggagca agataccgga gtggtacgag     120
gcgggaatat ccgccatttg gattcctccc gcgagcaagg gtatgagcgg cggctattcg     180
atgggctacg acccctacga ttattttgac ctcggtgagt actaccagaa gggaacggtg     240
gaaacgaggt tcggctcaaa gcaggagctc ataaacatga taaacacggc ccatgcctac     300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat     420
actgccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac     600
gtcaagggct atgctccctg ggtcgtcaag gactggctga actggtgggg aggctgggcg     660
gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt     720
gccaaggtct ttgacttcgc cctctactac aagatggacg cggcctttga caacaagaac     780
attcccgcac tcgtcgaggc cctcaagaac gggggcacag tcgtcagccg cgacccgttt     840
aaggccgtaa ccttcgttgc aaaccacgac accgatataa tctggaacaa gtatccagcc     900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
```

```
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga    1020
agcactgaca tcgtttacta cgacaacgac gagctgatat tcgtgagaaa cggctacgga    1080
agcaagccgg gactgataac atacatcaac ctcgcgtcaa gcaaagccgg aaggtgggtt    1140
tacgttccga agttcgcagg ctcgtgcata cacgagtaca ccggcaatct cggcggctgg    1200
gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg    1260
gccaacggcc agtacggcta ctccgtctgg agctactgcg gtgttgggtg a             1311

<210> 28
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 28
Met Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Ser Lys Ile Pro Glu Trp Tyr Glu Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Ala Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
```

```
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Ala Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 29
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 29

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atggccaagt acctggagct cgaagagggc gggctcataa tgcaggcctt ctactgggac      60
gtccccatgg gaggaatctg gtgggacacg gtagcccaga agatacccga ctgggcaagc     120
gccgggattt cggcgatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacacggc ccatgcctac     300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggtctc gggcaaatat     420
actgccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac     600
gtcaagggct atgctccctg ggtcgtcaag gactggctga actggtgggg aggctgggcg     660
gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt     720
gccaaggtct ttgacttcgc cctctactac aagatggatg aggcctttga caacaaaaac     780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc     840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtaccttgct     900
tatgccttca tcctcaccta cgaaggccag cccgtcatat tctaccgcga ctacgaggag     960
tggctcaaca aggacaggtt gaacaacctc atatggatac acgaccacct cgcaggggga    1020
agcaccgaca tagtctacta cgataacgat gaactcatct tcgtcaggaa cggctacggg    1080
gacaagccgg ggcttataac ctacatcaac ctaggctcga gcaaggccgg aaggtgggtt    1140
tatgtgccga agttcgcggg cgcgtgcatc cacgagtata ctggtaacct cggaggctgg    1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct    1260
gccaacgggc agtatggcta ctccgtgtgg agctactgcg gtgttgggtg a             1311
```

<210> 30
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 30

```
Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Leu Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Met Gly Gly Ile Trp Trp Asp Thr Val Ala
            20                  25                  30
Gln Lys Ile Pro Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Val Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Leu Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Arg Leu Asn Asn Leu Ile Trp Ile His Asp His
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 31
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 31
atggcaaagt actccgagct ggaagagggc ggcgttataa tgcaggcctt ctactgggac 60
gtcccaggtg gaggaatctg gtgggacacc atcaggagca ggataccgga gtggtacgag 120
gcgggaatat ccgccatttg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg 180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta 240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacacggc ccatgcctac 300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg 360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat 420
actgccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt 480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc 540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg ctttgactac 600
gtgaagggct acggagcgtg ggtcgtcaag gactggctca actggtgggg cggctgggcc 660
gttggcgagt actgggacac caacgttgat gcactcctca actgggccta ctcgagcggc 720
gccaaggtct tcgacttccc gctctactac aagatggacg aggccttcga taacaacaac 780
attcccgccc tggtggacgc cctcagatac ggtcagacag tggtcagccg cgacccgttc 840
aaggctgtga cgtttgtagc caaccacgat accgatataa tctggaacaa gtatccagcc 900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag 960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct ggccggagga 1020
agcacgagca tagtttacta cgacagcgac gagatgatct tcgtgaggac cggctatgga 1080
agcaagcctg gccttataac ttacatcaac ctcggctcga gcaaggttgg aaggtgggtt 1140
tatgtgccga agttcgcggg cgcgtgcatc cacgagtata ctggtaacct cggaggctgg 1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct 1260
gccaacgggc agtatggcta ctccgtgtgg agctattgcg gtgttggctg a 1311

<210> 32
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 32
Met Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
1 5 10 15
Phe Tyr Trp Asp Val Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Arg
20 25 30
Ser Arg Ile Pro Glu Trp Tyr Glu Ala Gly Ile Ser Ala Ile Trp Ile
35 40 45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
50 55 60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65 70 75 80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
85 90 95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
100 105 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
115 120 125

```
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Asn Asn Ile Pro Ala Leu Val Asp Ala Leu Arg Tyr Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
            340                 345                 350
Ile Phe Val Arg Thr Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 33
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 33

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atggccaagt actccgagct ggaagagggc ggggtcataa tgcaggcgtt ctactgggac      60
gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat     120
gccggaatct ccgcaatatg gattcctccc gcgagcaagg gtatgagcgg cggctattcg     180
atgggctacg acccctacga ttattttgac ctcggtgagt actaccagaa gggaacggtg     240
gaaacgaggt tcggctcaaa gcaggagctc ataaacatga taaacacggc ccatgcctac     300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat     420
```

```
actgccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg ctttgactac     600
gtgaagggct acggagcgtg ggtcgtcaag gactggctca actggtgggg cggctgggcc     660
gttggcgagt actgggacac caacgttgat gcactcctca actgggccta ctcgagcggc     720
gccaaggtct tcgactttcc gctctactac aagatggacg cggcctttga caacaagaac     780
attcccgcac tcgtcgaggc cctcaagaac gggggcacag tcgtcagccg cgacccgttt     840
aaggccgtaa ccttcgttgc aaaccacgac accgatataa tctggaccaa gtaccttgct     900
tatgctttca tcctcaccta cgaaggccag cccgtcatat tctaccgcga ctacgaggag     960
tggctcaaca aggacaggtt gaacaacctc atatggatac acgaccacct cgcaggtgga    1020
agcaccgaca tagtctacta cgataacgat gaactcatct tcgtcaggaa cggctacggg    1080
gacaagccgg ggcttataac ctacatcaac ctaggctcga gcaaggccgg aaggtgggtt    1140
tacgttccga agttcgcagg ctcgtgcata cacgagtaca ccggcaatct cggcggctgg    1200
gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg    1260
gccaacggcc agtacggcta ctccgtctgg agctactgcg gtgttggctg a              1311
```

<210> 34
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 34

```
Met Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe
                245                 250                 255
```

```
Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Thr Lys Tyr Leu Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Arg Leu Asn Asn Leu Ile Trp Ile His Asp His
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 35
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 35

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atggccaagt actccgagct ggaagagggc ggcgttataa tgcaggcctt ctactgggac      60
gtcccaggtg gaggaatctg gtgggacacc atcaggagca agataccgga gtggtacgag     120
gcgggaatat ccgccatttg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacaccgc ccacgcctac     300
ggcatcaagg tcatcgcaga catagtaatc aaccaccgcg ccggaggaga ccttgagtgg     360
aacccccttcg tcaatgacta cacctggacg gacttctcga aggtcgcttc cggcaagtac     420
acggccaact acctcgactt ccaccccaac gaggtcaagt gctgtgacga gggcacattt     480
ggaggcttcc cagacatagc ccacgagaag agctgggacc agcactggct ctgggcgagc     540
gatgagagct acgccgccta cctaaggagc atcggcgttg atgcctggcg cttcgactac     600
gtcaagggct atgctccctg ggtcgtcaag gactggctga actggtgggg aggctgggcg     660
gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt     720
gccaaggtct ttgacttcgc cctctactac aagatggacg cggcctttga caacaagaac     780
attcccgcac tcgtcgaggc cctcaagaac gggggcacag tcgtcagccg cgacccgttt     840
aaggccgtaa ccttcgttgc aaaccacgac accgatataa tctggaacaa gtatccagcc     900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacgt cgccggagga    1020
agcaccgaca tagtctacta cgataacgat gaactcatct tcgtcaggaa cggctacggg    1080
gacaagccgg ggcttataac ctacatcaac ctaggctcga gcaaggccgg aaggtgggtt    1140
tacgttccga agttcgcagg ctcgtgcata cacgagtaca ccggcaatct cggcggctgg    1200
gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg    1260
gccaacggcc agtacggcta ctccgtctgg agctactgcg gtgttgggtg a             1311
```

<210> 36
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 36
Met Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
1 5 10 15
Phe Tyr Trp Asp Val Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Arg
20 25 30
Ser Lys Ile Pro Glu Trp Tyr Glu Ala Gly Ile Ser Ala Ile Trp Ile
35 40 45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
50 55 60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65 70 75 80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
85 90 95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
100 105 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
115 120 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
130 135 140
Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe
145 150 155 160
Gly Gly Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln His Trp
165 170 175
Leu Trp Ala Ser Asp Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
180 185 190
Val Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
195 200 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
210 215 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225 230 235 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Ala Ala Phe
245 250 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
260 265 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
275 280 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
290 295 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305 310 315 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
325 330 335
Val Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
340 345 350
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr
355 360 365
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
370 375 380

```
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 37
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 37
atggccaagt acctggagct cgaagagggc ggggtcataa tgcaggcgtt ctactgggac 60
gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat 120
gccggaatct ccgcaatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg 180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta 240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacaccgc ccacgcctat 300
ggcatgaagg taatagccga tatagtcatc aaccaccgcg ccggcggtga cctggagtgg 360
aacccccttcg tgaacgacta tacctggacc gacttctcaa aggtcgcgtc gggtaaatac 420
acggccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt 480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc 540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg ctttgactac 600
gtgaagggct acggagcgcg ggtcgtcaag gactggctca actggtgggg cggctgggcc 660
gttggcgagt actgggacac caacgttgat gcactcctca actgggccta ctcgagcggc 720
gccaaggtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac 780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc 840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtatccagcc 900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctatcgcga ctacgaggag 960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga 1020
agcactgaca tcgtttacta cgacaacgac gagctgatat tcgtgagaaa cggctacgga 1080
agcaagccgg gactgataac atacatcaac ctcgcctcaa gcaaagccgg aaggtgggtt 1140
tacgttccga agttcgcagg ctcgtgcata cacgagtaca ccggcaatct cggcggctgg 1200
gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg 1260
gccaacggcc agtacggcta ctccgtctgg agctactgcg gggtggggtg a 1311

<210> 38
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 38
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Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
```

```
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Arg Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Ala Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 39
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 39
atggccaagt acctggagct cgaagagggc ggggtcataa tgcaggcgtt ctactgggac 60
gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat 120
gccggaatct ccgcaatatg gattcctccc gcgagcaggg gtatgagcgg cggctattcg 180
atgggctacg acccctacga ttattttgac ctcggtgagt actaccagaa gggaacggtg 240
gaaacgaggt tcggctcaaa gcaggagctc ataaacatga taaacaccgc ccacgcctat 300
ggcatgaagg taatagccga tatagtcatc aaccaccgcg ccggcggtga cctggagtgg 360
aacccttcg tgaacgacta tacctggacc gacttctcaa aggtcgcgtc gggtaaatac 420
acggccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt 480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc 540
caggagagct acgcggcata tctcaggagc atcggtatcg atgcctggcg ctttgactac 600
gtgaagggct acggagcgtg ggtcgtcaag gactggctca actggtgggg cggctgggcc 660
gttggcgagt actgggaccc caacgttgat gccctcctcc cctgggccta ctcgagcggc 720
gccaaggtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac 780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc 840
aaggccgtaa cctttgtagc caaccacgat accgatataa tctggaacaa gtatccagcc 900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag 960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga 1020
agcaccgaca tagtctacta cgataacgat gaactcatct tcgtcaggaa cggctacggg 1080
gacaagccgg ggcttataac ctacatcaac ctaggctcga gcaaggccgg aaggtgggtc 1140
tacgttccga agttcgcggg agcgtgcatc cacgagtaca ccggcaacct cggcggctgg 1200
gtggacaagt gggtggactc aagcgggtgg gtgtacctcg aggcccctgc ccacgacccg 1260
gccaacggct attacggcta ctccgtctgg agctactgcg gggtgggctg a 1311

<210> 40
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 40
Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1   5   10   15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20   25   30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
        35   40   45
Pro Pro Ala Ser Arg Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
    50   55   60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65   70   75   80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
                85   90   95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
            100   105   110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
        115   120   125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130   135   140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145   150   155   160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165   170   175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly

```
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Pro Asn Val Asp Ala Leu Leu Pro Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 41
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 41

```
atggccaagt acctggagct cgaagagggc ggggtcataa tgcaggcgtt ctactgggac      60
gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat     120
gccggaatct ccgcaatatg gattcctccc gcgagcaagg gtatgagcgg cggctattcg     180
atgggctacg acccctacga ttattttgac ctcggtgagt actaccagaa gggaacggtg     240
gaaacgaggt tcggctcaaa gcaggagctc ataaacatga taaacacggc ccatgcctac     300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat     420
actgccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg ctttgactac     600
gtgaagggct acggagcgtg ggtcgtcaag gactggctca actggtgggg cggctgggcc     660
gttggcgagt actgggacac caacgttgat gcactcctca actgggccta ctcgagcggc     720
gccaaggtct tcgacttccc gctctactac aagatggacg cggcctttga caacaagaac     780
attcccgcac tcgtcgaggc cctcaagaac gggggcacag tcgtcagccg cgacccgttt     840
```

```
aaggccgtaa ccttcgttgc aaaccacgac accgatataa tctggaacaa gtatccagcc     900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga    1020
agcacgagca tagtttacta cgacagcgac gagatgatct tcgtgaggaa cggctatgga    1080
agcaagcctg gccttataac ttacatcaac ctcggctcga gcaaggttgg aaggtgggtt    1140
tatgtgccga agttcgcggg cgcgtgcatc cacgagtata ctggtaacct cggaggctgg    1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct    1260
gccaacgggc agtatggcta ctccgtgtgg agctactgcg gtgttgggtg a              1311

<210> 42
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 42
Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
```

```
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 43
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 43

```
atggccaagt actccgagct ggaagagggc ggcgttataa tgcaggcctt ctactgggac      60
gtcccaggtg gaggaatctg gtgggacacc atcaggagca agataccgga gtggtacgag     120
gcgggaatat ccgccatttg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacacggc ccatgcctac     300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat     420
actgccaact acctcgactt ccaccccaac gaggtcaagt gctgtgacga gggcacattt     480
ggaggcttcc cagacatagc ccacgagaag agctgggacc agcactggct ctgggcgagc     540
gatgagagct acgccgccta cctaaggagc atcggcgttg atgcctggcg cttcgactac     600
gtcaagggct acggagcgtg ggtcgtcaag gactggctgg actggtgggg aggctgggcc     660
gtcggggagt actgggacac aaacgttgat gcactgctca actgggccta ctcgagcgat     720
gcaaaagtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac     780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc     840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtatccagcc     900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgtcggagga    1020
agcacgagca tagtttacta cgacagcgac gagatgatct tcgtgaggaa cggctatgga    1080
agcaagcctg gccttataac ttacatcaac ctcggctcga gcaaggttgg aaggtgggtt    1140
tacgttccga agttcgcagg ctcgtgcata cacgagtaca ccggcaatct cggcggctgg    1200
gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg    1260
gccaacggcc agtacggcta ctccgtctgg agctactgcg gtgttggctg a             1311
```

<210> 44
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 44

```
Met Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Ser Lys Ile Pro Glu Trp Tyr Glu Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe
145                 150                 155                 160
Gly Gly Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln His Trp
                165                 170                 175
Leu Trp Ala Ser Asp Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Val Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asp Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Asp
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Val Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
```

435

<210> 45
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 45
atggccaagt actccgacct ggaagagggc ggcgttataa tgcaggcctt ctactgggac 60
gtcccaggtg gaggaatctg gtgggacacc atcaggagca agataccgga gtggtacgag 120
gcgggaatat ccgccatttg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg 180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta 240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacacggc ccatgcctac 300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg 360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat 420
actgccaact acctcgactt ccaccccaac gaggtcaagt gctgtgacga gggcacattt 480
ggaggcttcc cagacatagc ccacgagaag agctgggacc agcactggct ctgggcgagc 540
gatgagagct acgccgccta cctaaggagc atcggcgttg atgcctggcg ctttgactac 600
gtgaagggct acggagcgtg ggtcgtcaag gactggctca actggtgggg cggctgggcc 660
gttggcgagt actgggacac caacgttgat gcactcctca actgggccta ctcgagcggc 720
gccaaggtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac 780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc 840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtatccagcc 900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag 960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga 1020
agcaccgaca tagtctacta cgataacgat gaactcatct tcgtcaggaa cggctacggg 1080
gacaagccgg ggcttataac ctacatcaac ctaggctcga gcaaggccgg aaggtgggtt 1140
tatgtgccga agttcgcggg cgcgtgcatc cacgagtata ctggtaacct cggaggctgg 1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct 1260
gccaacgggc agtatggcta ctccgtgtgg agctattgcg gtgttgggtg a 1311

<210> 46
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 46
Met Ala Lys Tyr Ser Asp Leu Glu Glu Gly Gly Val Ile Met Gln Ala
1 5 10 15
Phe Tyr Trp Asp Val Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Arg
20 25 30
Ser Lys Ile Pro Glu Trp Tyr Glu Ala Gly Ile Ser Ala Ile Trp Ile
35 40 45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
50 55 60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65 70 75 80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
85 90 95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
100 105 110

```
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe
145                 150                 155                 160
Gly Gly Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln His Trp
                165                 170                 175
Leu Trp Ala Ser Asp Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Val Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 47
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 47

```
atggccaagt acaccgagct ggaagagggc ggcgttataa tgcaggcctt ctactgggac      60
gtcccaggtg gaggaatctg gtgggacacc atcaggagca agataccgga gtggtacgag     120
gcgggaatat ccgccatttg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacaccgc ccacgcctat     300
```

```
ggcatgaagg taatagccga tatagtcatc aaccaccgcg ccggcggtga cctggagtgg     360
aacccttcg tgaacgacta tacctggacc gacttctcaa aggtcgcgtc gggtaaatac     420
acggccaact acctcgactt ccaccccaac gaggtcaagt gctgtgacga gggcacattt     480
ggaggcttcc cagacatagc ccacgagaag agctgggacc agcactggct ctgggcgagc     540
gatgagagct acgccgccta cctaaggagc atcggcgttg atgcctggcg ctttgactac     600
gtgaagggct acggagcgtg ggtcgtcaag gactggctca actggtgggg cggttgggcc     660
gttggcgagt actgggacac caacgttgat gcactcctca actgggccta ctcgagcggc     720
gccaaggtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac     780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc     840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtaccttgct     900
tatgctttca tcctcaccta cgaaggccag cccgtcatat tctaccgcga ctacgaggag     960
tggctcaaca aggacaggtt gaacaacctc atatggatac acgaccacct cgcaggtgga    1020
agcacgagca tagtttacta cgacagcgac gagatgatct tcgtgaggaa cggctatgga    1080
agcaagcctg gccttataac ttacatcaac ctcggctcga gcaaggttgg aaggtgggtt    1140
tacgttccga agttcgcagg cccgtgcata cacgagtaca ccggcaatct cggcggctgg    1200
gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg    1260
gccaacggcc agtacggcta ctccgtctgg agctactgcg gtgttgggta g              1311
```

<210> 48
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 48

```
Met Ala Lys Tyr Thr Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Ser Lys Ile Pro Glu Trp Tyr Glu Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe
145                 150                 155                 160
Gly Gly Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln His Trp
                165                 170                 175
Leu Trp Ala Ser Asp Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Val Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
```

```
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Leu Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Arg Leu Asn Asn Leu Ile Trp Ile His Asp His
                325                 330                 335
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Pro Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 49
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 49

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gtggtttatg acgatgtccg ctatgacctt tatgccgtag gcatgggccg tgtttatcat      60
gttcacgagc tcctgcttgg agccaaagcg cgtctctacc gttcccttct ggtcgtactc     120
accgaggtca aagaagtcgt aggggtcgta gcccatcgaa taggcgccgc ccatgccctt     180
gctcgccggg ggaatccata tcgccgaaat cccggcgctt gcccagtcgg gtatcttctg     240
ggctatcgtg tcccaccaga ttcctcccat ggggacgtcc cagtagaagg cctgcattat     300
gagcccgccc tcttcgagcc cggaatactt tgccataagt tacctcctac tagtagatta     360
aaattctgtt tcctgtgtga aattgtt                                        387
```

<210> 50
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 50

```
Val Val Tyr Asp Asp Val Arg Tyr Asp Leu Tyr Ala Val Gly Met Gly
 1               5                  10                  15
Arg Val Tyr His Val His Glu Leu Leu Leu Gly Ala Lys Ala Arg Leu
            20                  25                  30
```

```
Tyr Arg Ser Leu Leu Val Val Leu Thr Glu Val Lys Glu Val Val Gly
        35                  40                  45
Val Val Ala His Arg Ile Gly Ala Ala His Ala Leu Ala Arg Arg Gly
    50                  55                  60
Asn Pro Tyr Arg Arg Asn Pro Gly Ala Cys Pro Val Gly Tyr Leu Leu
65                  70                  75                  80
Gly Tyr Arg Val Pro Pro Asp Ser Ser His Gly Asp Val Pro Val Glu
                85                  90                  95
Gly Leu His Tyr Glu Pro Ala Leu Phe Glu Pro Gly Ile Leu Cys His
            100                 105                 110
Lys Leu Pro Pro Thr Ser Arg Leu Lys Phe Cys Phe Leu Cys Glu Ile
        115                 120                 125
Val
```

<210> 51
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 51

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atggccaagt acctggagct cgaagagggc ggggtcataa tgcaggcgtt ctactgggac      60
gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat     120
gccggaatct ccgcaatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacaccgc ccacgcctat     300
ggcatgaagg taatagccga tatagtcatc aaccaccgcg ccggcggtga cctggagtgg     360
aacccttcg tgaacgacta tacctggacc gacttctcaa aggtcgcgtc gggtaaatac     420
acggccaact acctcgactt ccaccccaac gaggtcaagt gctgtgacga gggcacattt     480
ggaggcttcc cagacatagc ccacgagaag agctgggacc agcactggct ctgggcgagc     540
gatgagagct acgccgccta cctaaggagc atcggcgttg atgcctggcg ctttgactac     600
gtgaagggct acggagcgtg ggtcgtcaag gactggctca actggtgggg cggctgggcc     660
gttggcgagt actgggacac caacgttgat gcactcctca actgggccta ctcgagcggc     720
gccaaggtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac     780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc     840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtatccagcc     900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga    1020
agcactgaca tcgtttacta cgacaacgac gagctgatat tcgtgagaaa cggctacgga    1080
agcaagccgg gactgataac atacatcaac ctcgcctcaa gcaaagccgg aaggtgggtt    1140
tacgttccga agttcgcagg ctcgtgcata cacgagtaca ccggcaatct cggcggctgg    1200
gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg    1260
gccaacggcc agtacggcta ctccgtctgg agctattgcg gtgttggctg a             1311
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<210> 52
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 52

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Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
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 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe
145                 150                 155                 160
Gly Gly Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln His Trp
                165                 170                 175
Leu Trp Ala Ser Asp Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Val Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Ala Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
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<210> 53

<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 53
atggccaagt actccgagct ggaagagggc ggcgttataa tgcaggcctt ctactgggac 60
gtcccaggtg gaggaatctg gtgggacacc atcaggagca agataccgga gtggtacgag 120
gcgggaatat ccgccatttg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg 180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta 240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacacggc ccatgcctac 300
ggcataaagg tcatagcgga catcgtcata aaccaccgca caggcggaga cctcgagtgg 360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat 420
actgccaact acctcgactt ccaccccaac gaggtcaagt gctgtgacga gggcacattt 480
ggaggcttcc cagacatagc ccacgagaag agctgggacc agcactggct ctgggcgagc 540
gatgagagct acgccgccta cctaaggagc atcggcgttg atgcctggcg cttcgactac 600
gtcaagggct acggagcgtg ggtcgtcaag gactggctgg actggtgggg aggctgggcc 660
gtcggggagt actgggacac aaacgttgat gcactgctca actgggccta ctcgagcgat 720
gcaaaagtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac 780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc 840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtatccagcc 900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag 960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga 1020
agcactgaca tcgtttacta cgacaacgac gagctgatat tcgtgagaaa cggctacgga 1080
agcaagccgg gactgataac atacatcaac ctcgcctcaa gcaaagccgg aaggtgggtc 1140
tacgttccga agttcgcggg agcgtgcatc cacgagtaca ccggcaacct cggcggctgg 1200
gtggacaagt gggtggactc aagcgggtgg gtgtacctcg aggcccctgc ccacgacccg 1260
gccaacggct attacggcta ctccgtctgg agctactgcg gtgttggctg a 1311

<210> 54
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 54
Met Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
1 5 10 15
Phe Tyr Trp Asp Val Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Arg
20 25 30
Ser Lys Ile Pro Glu Trp Tyr Glu Ala Gly Ile Ser Ala Ile Trp Ile
35 40 45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
50 55 60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65 70 75 80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
85 90 95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
100 105 110
Arg Thr Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
115 120 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr

```
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe
145                 150                 155                 160
Gly Gly Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln His Trp
                165                 170                 175
Leu Trp Ala Ser Asp Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Val Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asp Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Asp
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Ala Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 55
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 55

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atggccaagt acctggagct cgaggagggc ggggtcataa tgcaggcgtt ctactgggac      60
gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat     120
gccggaatct ccgcaatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacaccgc ccacgcctat     300
ggcatgaagg taatagccga tatagtcatc aaccaccgcg ccggcggtga cctggagtgg     360
aacccccttcg tgaacgacta tacctggacc gacttctcaa aggtcgcgtc gggtaaatac     420
acggccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
```

```
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg ctttgactac     600
gtgaagggct acggagcgtg ggtcgtcaag gactggctca actggtgggg cggctgggcc     660
gttggcgagt actgggacac caacgttgat gcactcctca actgggccta ctcgagcggc     720
gccaaggtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac     780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc     840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtaccttgct     900
tatgctttca tcctcaccta cgaaggccag cccgtcatat tctaccgcga ctacgaggag     960
tggctcaaca aggacaggtt gaacaacctc atatggatac acgaccacct cgcaggtgga    1020
agcacgagca tagtttacta cgacagcgac gagatgatct tcgtgaggaa cggctatgga    1080
agcaagcctg gccttataac ttacatcaac ctcggctcga gcaaggttgg aaggtgggtt    1140
tacgttccga agttcgcagg ctcgtgcata cacgagtaca ccggcaatct cggcggctgg    1200
gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg    1260
gccaacggcc agtacggcta ctccgtctgg agctattgcg gtgttggctg a             1311

<210> 56
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 56
Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
```

```
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Leu Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Arg Leu Asn Asn Leu Ile Trp Ile His Asp His
                325                 330                 335
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 57
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 57

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atggccaagt acctggagct cgaagagagc ggggtcataa tgcaggcgtt ctactgggac      60
gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat     120
gccggaatct ccgcaatatg gattcctccc gcgagcaagg gtatgagcgg cggctattcg     180
atgggctacg acccctacga ttattttgac ctcggtgagt actaccagaa gggaacggtg     240
gaaacgaggt tcggctcaaa gcaggagctc ataaacatga taaacaccgc ccacgcctac     300
ggcatcaagg tcatcgcaga catagtaatc aaccaccgcg ccggaggaga ccttgagtgg     360
aacccttcg tcaatgacta cacctggacg gacttctcga aggtcgcttc cggcaagtac      420
acggccaact acctcgactt ccaccccaac gaggtcaagt gctgtgacga gggcacattt     480
ggaggcttcc cagacatagc ccacgagaag agctgggacc agcactggct ctgggcgagc     540
gatgagagct acgccgccta cctaaggagc atcggcgttg atgcctggcg ctttgactac     600
gtgaagggct acggagcgtg ggtcgtcaag gactggctca actggtgggg tggctgggcc     660
gtcggggagt actgggacac aaacgttgat gcactgctca actgggccta ctcgagcgat     720
gcaaaagtct tcgacttccc gctctactac aagatggacg aggccttcga taacaacaac     780
attcccgccc tggtggacgc cctcagatac ggtcagacag tggtcagccg cgacccgttc     840
aaggctgtga cgtttgtagc caaccacgat accgatataa tctggaacaa gtaccttgct     900
tatgctttca tcctcaccta cgaaggccag cccgtcatat tctaccgcga ctacgaggag     960
tggctcaaca aggacaggtt gaacaacctc atatggatac acgaccacct cgcaggtgga    1020
agcactgaca tcgtttacta cgacaacgac gagctgatat tcgtgagaaa cggctacgga    1080
agcaagccgg gactgataac atacatcaac ctcgcctcaa gcaaagccgg aaggtgggtc    1140
tacgttccga agttcgcggg agcgtgcatc cacgagtaca ccggcaacct cggcggctgg    1200
gtggacaagt gggtggactc aagcgggtgg gtgtacctcg aggcccctgc ccacgacccg    1260
gccaacggct attacggcta ctccgtctgg agctattgcg gtgttggctg a             1311
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<210> 58

<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 58
Met Ala Lys Tyr Leu Glu Leu Glu Glu Ser Gly Val Ile Met Gln Ala
 1   5   10   15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20   25   30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
        35   40   45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
    50   55   60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65   70   75   80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
                85   90   95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100   105   110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
        115   120   125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130   135   140
Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe
145   150   155   160
Gly Gly Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln His Trp
                165   170   175
Leu Trp Ala Ser Asp Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180   185   190
Val Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195   200   205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210   215   220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Asp
225   230   235   240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245   250   255
Asp Asn Asn Asn Ile Pro Ala Leu Val Asp Ala Leu Arg Tyr Gly Gln
            260   265   270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275   280   285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Leu Ala Tyr Ala Phe Ile
    290   295   300
Leu Thr Tyr Glu Gly Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu
305   310   315   320
Trp Leu Asn Lys Asp Arg Leu Asn Asn Leu Ile Trp Ile His Asp His
                325   330   335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340   345   350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355   360   365
Ile Asn Leu Ala Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370   375   380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp

385 390 395 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
405 410 415
Ala His Asp Pro Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr
420 425 430
Cys Gly Val Gly
435

<210> 59
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 59
atggccaagt acctggagct cgaagagggc ggggtcataa tgcaggcgtt ctactgggac 60
gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat 120
gccggaatct ccgcaatatg gattcctccc gcgagcaagg gtatgagcgg cggctattcg 180
atgggctacg acccctacga ttattttgac ctcggtgagt actaccagaa gggaacggtg 240
gaaacgaggt tcggctcaaa gcaggagctc ataaacatga taaacaccgc ccacgcctac 300
ggcatcaagg tcatcgcaga catagtaatc aaccaccgcg ccggaggaga ccttgagtgg 360
aacccttcg tcaatgacta cacctggacg gacttctcga aggtcgcttc cggcaagtac 420
acggccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt 480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc 540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac 600
gtcaagggct atgctccctg ggtcgtcaag gactggctga actggtgggg aggctgggcg 660
gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt 720
gccaaggtct ttgacttcgc cctctactac aagatggacg aggccttcga taacaacaac 780
attcccgccc tggtggacgc cctcagatac ggtcagacag tggtcagccg cgacccgttc 840
aaggctgtga cgtttgtagc caaccacgat accgatataa tttggaacaa gtacccggcc 900
tacgccttca tcctcaccta cgagggccag ccgacgatat tctaccgcga ctacgaggag 960
tggctcaaca aggacaggct caagaacctc atctggatac acgaccacct cgccggtgga 1020
agcactgaca tcgtttacta cgacaacgac gagctgatat tcgtgagaaa cggctacgga 1080
agcaagccgg gactgataac atacatcaac ctcgcgtcaa gcaaagccgg aaggtgggtt 1140
tatgtgccga agttcgcggg cgcgtgcatc cacgagtata ctggtaacct cggaggctgg 1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct 1260
gccaacgggc agtatggcta ctccgtgtgg agctattgcg gtgttgggtg a 1311

<210> 60
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 60
Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
1 5 10 15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
20 25 30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
35 40 45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
50 55 60

```
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Asn Asn Ile Pro Ala Leu Val Asp Ala Leu Arg Tyr Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Arg Leu Lys Asn Leu Ile Trp Ile His Asp His
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Ala Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
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<210> 61
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 61
atggccaagt actccgagct gaaaaagggc ggggtcataa tgcaggcgtt ctactgggac 60
gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgag 120
gcgggaatat ccgccatttg gattcctccc gcgagcaagg gtatgagcgg cggctattcg 180
atgggctacg acccctacga ttattttgac ctcggtgagt actaccagaa gggaacggtg 240
gaaacgaggt tcggctcaaa gcaggagctc ataaacatga taaacaccgc ccacgcctac 300
ggcatcaagg tcatcgcaga catagtaatc aaccaccgcg ccggaggaga ccttgagtgg 360
aacccttcg tcaatgacta cacctggacg gacttctcga aggtcgcttc cggcaagtac 420
acggccaact acctcaactt ccacccgaac gagctccatg cgggcgattc cggaacattt 480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc 540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac 600
gtcaagggct acggagcgtg ggtcgtcaag gactggctgg actggtgggg aggctgggcc 660
gtcggggagt actgggacac aaacgttgat gcactgctca actgggccta ctcgagcgat 720
gcaaaagtct tcgacttccc gctctactac aagatggatg aggcctttga caacaaaaac 780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc 840
aaggccgtaa cctttgtagc aaaccatgac accgatataa tctggaacaa gtatccagcc 900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag 960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga 1020
agcaccgaca tagtctacta cgataacgat gaactcatct tcgtcaggaa cggctacggg 1080
gacaagccgg ggcttataac ctacatcaac ctaggctcga gcaaggccgg aaggtgggtc 1140
tacgttccga agttcgcggg agcgtgcatc cacgagtaca ccggcaacct cggcggctgg 1200
gtggacaagt gggtggactc aagcgggtgg gtgtacctcg aggcccctgc ccacgacccg 1260
gccaacggct attacggcta ctccgtctgg agctactgcg gggtgggctg a 1311

<210> 62
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 62
Met Ala Lys Tyr Ser Glu Leu Lys Lys Gly Gly Val Ile Met Gln Ala
1 5 10 15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
20 25 30
Gln Lys Ile Pro Glu Trp Tyr Glu Ala Gly Ile Ser Ala Ile Trp Ile
35 40 45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
50 55 60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65 70 75 80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
85 90 95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
100 105 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
115 120 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
130 135 140
Leu Asn Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145 150 155 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
165 170 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
180 185 190

```
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asp Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Asp
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
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<210> 63
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 63

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atggccaagt acctggagct cgaagagggc ggggtcataa tgcaggcgtt ctactgggac      60
gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat     120
gccggaatct ccgcaatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacacggc ccatgcctac     300
ggcataaagg ccatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat     420
actgccaact acctcgactt ccaccccaac gaggtcaagt gctgtgacga gggcacattt     480
ggaggcttcc cagacatagc ccacgagaag agctgggacc agcactggct ctgggcgagc     540
gatgagagct acgccgccta cctaaggagc atcggcgttg atgcctggcg ctttgactac     600
gtgaagggct acggagcgtg ggtcgtcaag gactggctca actggtgggg cggctgggcc     660
gttggcgagt actgggacac caacgttgat gcactcctca actgggccta ctcgagcggc     720
gccaaggtct tcgacttccc gctctactac aagatggacg cggcctttga caacaagaac     780
attcccgcac tcgtcgaggc cctcaagaac gggggcacag tcgtcagccg cgacccgttt     840
aaggccgtaa ccttcgttgc aaaccacgac accgatataa tctggaacaa gtatccagcc     900
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```
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga    1020
agcaccgaca tagtctacta cgataacgat gaactcatct tcgtcaggaa cggctacggg    1080
gacaagccgg ggcttataac ctacatcaac ctaggctgga gcaaggccgg aaggtgggtt    1140
tatgtgccga agttcgcggg cgcgtgcatc cacgagtata ctggtaacct cggaggctgg    1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct    1260
gccaacgggc agtatggcta ctccgtgtgg agctactgcg gggtggggtg a             1311

<210> 64
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 64
Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Ala Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe
145                 150                 155                 160
Gly Gly Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln His Trp
                165                 170                 175
Leu Trp Ala Ser Asp Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Val Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
```

```
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Trp Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 65
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 65

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atggccaagt actccgagct ggaagaaggc ggcgttataa tgcaggcctt ctactgggac      60
gtcccaggtg gaggaatctg gtggggcacc atcaggagca agataccgga gtggtacgag     120
gcgggaatat ccgccatttg gattcctccc gcgagcaagg gtatgagcgg cggctattcg     180
atgggctacg acccctacga ttattttgac ctcggtgagt actaccagaa gggaacggtg     240
gaaacgaggt tcggctcaaa gcaggagctc ataaacatga taaacaccgc ccacgcctat     300
ggcatgaagg taatagccga tatagtcatc aaccaccgcg ccggcggtga cctggagtgg     360
aaccccttcg tgaacgacta tacctggacc gacttctcaa aggtcgcgtc gggtaaatac     420
acggccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac     600
gtcaagggct atgctccctg ggtcgtcaag gactggctga actggtgggg aggctgggcg     660
gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt     720
gccaaggtct ttgacttcgc cctctactac aagatggacg aggccttcga taacaacaac     780
attcccgccc tggtggacgc cctcagatac ggtcagacag tggtcagccg cgacccgttc     840
aaggctgtga cgtttgtagc caaccacgat accgatataa tttggaacaa gtacccggcc     900
tacgccttca tcctcaccta cgagggccag ccgacgatat tctaccgcga ctacgaggag     960
tggctcaaca aggacaggct caagaacctc atctggatac acgaccacct cgccggtgga    1020
agcacgagca tagtttacta cgacagcgac gagatgatct tcgtgaggaa cggctatgga    1080
agcaagcctg gccttataac ttacatcaac ctcggctcga gcaaggttgg aaggtgggtt    1140
tacgttccga agttcgcagg ctcgtgcata cacgagtaca ccggcaatct cggcggctgg    1200
gtggacaagt gggtggactc aagcggctgg gtctacctcg aggctcctgc ccacgacccg    1260
gccaacggcc agtacggcta ctccgtctgg agctattgcg gtgttggctg a             1311
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<210> 66
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 66

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Met Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Gly Gly Gly Ile Trp Trp Gly Thr Ile Arg
            20                  25                  30
Ser Lys Ile Pro Glu Trp Tyr Glu Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Asn Asn Ile Pro Ala Leu Val Asp Ala Leu Arg Tyr Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Arg Leu Lys Asn Leu Ile Trp Ile His Asp His
                325                 330                 335
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
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<210> 67
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 67
atggccaagt acctggagct cgaagagggc ggggtcataa tgcaggcgtt ctactgggac 60
gtgccttcgg gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat 120
gccggaatct ccgcaatatg gattcctccc gcgagcaagg gtatgagcgg cggctattcg 180
atgggctacg acccctacga ttattttgac ctcggtgagt actaccagaa gggaacggtg 240
gaaacgaggt tcggctcaaa gcaggagctc ataaacatga taaacacggc ccatgcctac 300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg 360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtggcctc gggcaaatat 420
actgccaact acctcgactt ccaccccaac gaggtcaagt gctgtgacga gggcacattt 480
ggaggcttcc cagacatagc ccacgagaag agctgggacc agcactggct ctgggcgagc 540
gatgagagct acgccgccta cctaaggagc atcggcgttg atgcctggcg cttcgactac 600
gtcaagggct acggagcgtg ggtcgtcaag gactggctgg actggtgggg aggctgggcc 660
gtcggggagt actgggacac aaacgttgat gcactgctca actgggccta ctcgagcgat 720
gcaaaagtct tcgacttccc gctctactac aagatggacg aggccttcga taacaacaac 780
attcccgccc tggtggacgc cctcagatac ggtcagacag tggtcagccg cgacccgttc 840
aaggctgtga cgtttgtagc caaccacgat accgatataa tctggaacaa gtatccagcc 900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag 960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga 1020
agcacgagca tagtttacta cgacagcgac gagatgatct tcgtgaggaa cggctatgga 1080
agcaagcctg gccttataac ttacatcaac ctcggctcga gcaaggttgg aaggtgggtc 1140
tacgttccga agttcgcggg agcgtgcatc cacgagtaca ccggcaacct cggcggctgg 1200
gtggacaagt gggtggactc aagcgggtgg gtgtacctcg aggcccctgc ccacgacccg 1260
gccaacggct attacggcta ctccgtctgg agctactgcg tggtgggctg a 1311

<210> 68
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 68
Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
1 5 10 15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
20 25 30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
35 40 45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
50 55 60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65 70 75 80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
85 90 95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
100 105 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr

```
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe
145                 150                 155                 160
Gly Gly Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln His Trp
                165                 170                 175
Leu Trp Ala Ser Asp Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Val Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asp Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Asp
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Asn Asn Ile Pro Ala Leu Val Asp Ala Leu Arg Tyr Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Trp Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala His Asp Pro Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Val Val Gly
        435
```

<210> 69
<211> 1542
<212> DNA
<213> Environmental

<400> 69

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atgttgaaaa ggattacggt agtctgttta ttgtttattt tgctttttcc taatatatat      60
gagggaaata aggcagaagc agcaacagtg aacaatggaa cattaatgca gtattttgag     120
tggtacgctc cgaatgatgg gaatcattgg aatcgtttgc gttccgatgc tgaaagttta     180
gctcataaag gaatcacatc tgtatggata ccacctgcat ataaagggac ttcgcaaaat     240
gatgtagggt atggggccta tgatttatat gatttagggg agttcaatca aaaaggaacg     300
gtgcggacga aatatgggac aaaagcacag ttgaaatctg caattgacgc tttacataag     360
caaaacatcg acgtatacgg tgatgtagtt atgaatcata aaggtggggc tgattatact     420
gaaaccgtaa cagctgttga ggtagaccgt aacaatcgaa atattgaagt atcaggtgat     480
tatcaaatta gtgcatggac ggggtttaat tttccagggc gcggagatgc ttattctaat     540
```

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ttcaaatgga aatggtatca ttttgacgga acggattggg atgaaggaag gaaattaaat     600
cgaatttata aatttagggg tgtagataaa gcgtgggatt gggaagtgtc tagcgaaaat     660
ggaaattatg attatttgat gtatgcagat cttgattttg atcatcctga tgttgcgaat     720
gagatgaaaa attggggaac atggtatgcg aatgaattaa atttagatgg ctttcgtttg     780
gacgctgtta aacatattga tcatgaatat ttacgcgatt gggtaaatca tgccagacag     840
caaacgggga aagaaatgtt tacagtagct gaatattggc aaaatgatgt tcaggcttta     900
aacaattatt tagcgaaagt caattataat caatctgtgt ttgatgcacc gcttcattac     960
aattttcatt atgcttcaac aggaaatggg aattatgata tgagaaatat tttaaatgga    1020
acagtaatga aaaatcaccc tgcactcgca gttactctcg ttgagaatca tgattctcag    1080
cctgggcagt cattggaatc tgtagtaagt ccgtggttta agccgctggc atatgcattt    1140
attttaactc gtgcagaggg ctatccttca gttttctatg gtgattacta tgggacaagc    1200
ggaaatagta gttatgaaat tccagcgtta aaagataaaa ttgatccaat tttgacggca    1260
cgaaaaaact ttgcatatgg tacgcagcgt gattatttag accatccaga tgtgattggc    1320
tggacaagag aaggcgatgg tgtacatgct aattctggtt tagcgacatt actctcggac    1380
ggaccaggag gatcaaagtg gatggatgtt ggaaagaata acgctgggga agtatggtac    1440
gatattacgg gtaatcaaac aaatactgta acaattaata aggacggatg ggggcagttc    1500
tatgtaagtg gcggctcagt ttccatatat gttcagcggt aa                       1542
```

<210> 70
<211> 513
<212> PRT
<213> Environmental

<400> 70

```
Met Leu Lys Arg Ile Thr Val Val Cys Leu Leu Phe Ile Leu Leu Phe
 1               5                  10                  15
Pro Asn Ile Tyr Glu Gly Asn Lys Ala Glu Ala Ala Thr Val Asn Asn
            20                  25                  30
Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Ala Pro Asn Asp Gly Asn
        35                  40                  45
His Trp Asn Arg Leu Arg Ser Asp Ala Glu Ser Leu Ala His Lys Gly
    50                  55                  60
Ile Thr Ser Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln Asn
65                  70                  75                  80
Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn
                85                  90                  95
Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln Leu Lys
            100                 105                 110
Ser Ala Ile Asp Ala Leu His Lys Gln Asn Ile Asp Val Tyr Gly Asp
        115                 120                 125
Val Val Met Asn His Lys Gly Gly Ala Asp Tyr Thr Glu Thr Val Thr
    130                 135                 140
Ala Val Glu Val Asp Arg Asn Asn Arg Asn Ile Glu Val Ser Gly Asp
145                 150                 155                 160
Tyr Gln Ile Ser Ala Trp Thr Gly Phe Asn Phe Pro Gly Arg Gly Asp
                165                 170                 175
Ala Tyr Ser Asn Phe Lys Trp Lys Trp Tyr His Phe Asp Gly Thr Asp
            180                 185                 190
Trp Asp Glu Gly Arg Lys Leu Asn Arg Ile Tyr Lys Phe Arg Gly Val
        195                 200                 205
Asp Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn Tyr Asp
    210                 215                 220
Tyr Leu Met Tyr Ala Asp Leu Asp Phe Asp His Pro Asp Val Ala Asn
225                 230                 235                 240
Glu Met Lys Asn Trp Gly Thr Trp Tyr Ala Asn Glu Leu Asn Leu Asp
                245                 250                 255
Gly Phe Arg Leu Asp Ala Val Lys His Ile Asp His Glu Tyr Leu Arg
```

```
            260                 265                 270
Asp Trp Val Asn His Ala Arg Gln Gln Thr Gly Lys Glu Met Phe Thr
        275                 280                 285
Val Ala Glu Tyr Trp Gln Asn Asp Val Gln Ala Leu Asn Asn Tyr Leu
    290                 295                 300
Ala Lys Val Asn Tyr Asn Gln Ser Val Phe Asp Ala Pro Leu His Tyr
305                 310                 315                 320
Asn Phe His Tyr Ala Ser Thr Gly Asn Gly Asn Tyr Asp Met Arg Asn
                325                 330                 335
Ile Leu Asn Gly Thr Val Met Lys Asn His Pro Ala Leu Ala Val Thr
            340                 345                 350
Leu Val Glu Asn His Asp Ser Gln Pro Gly Gln Ser Leu Glu Ser Val
        355                 360                 365
Val Ser Pro Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
    370                 375                 380
Ala Glu Gly Tyr Pro Ser Val Phe Tyr Gly Asp Tyr Tyr Gly Thr Ser
385                 390                 395                 400
Gly Asn Ser Ser Tyr Glu Ile Pro Ala Leu Lys Asp Lys Ile Asp Pro
                405                 410                 415
Ile Leu Thr Ala Arg Lys Asn Phe Ala Tyr Gly Thr Gln Arg Asp Tyr
            420                 425                 430
Leu Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Gly Val
        435                 440                 445
His Ala Asn Ser Gly Leu Ala Thr Leu Leu Ser Asp Gly Pro Gly Gly
    450                 455                 460
Ser Lys Trp Met Asp Val Gly Lys Asn Asn Ala Gly Glu Val Trp Tyr
465                 470                 475                 480
Asp Ile Thr Gly Asn Gln Thr Asn Thr Val Thr Ile Asn Lys Asp Gly
                485                 490                 495
Trp Gly Gln Phe Tyr Val Ser Gly Gly Ser Val Ser Ile Tyr Val Gln
            500                 505                 510
Arg
```

<210> 71
<211> 1311
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated oligonucleotide

<400> 71

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atggccaagt acctggagct cgaagagggc ggggtcataa tgcaggcgtt ctactgggac      60
gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat     120
gccggaatct ccgcaatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacacggc ccatgcctac     300
ggcataaagg tcatagcgga catcgtcata aaccaccgcg caggcggaga cctcgagtgg     360
aacccgttcg ttggggacta cacctggacg gacttctcaa aggtagcctc gggcaaatat     420
actgccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac     600
gtcaagggct atgctccctg ggtcgtcaag gactggctga actggtgggg aggctgggcg     660
gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt     720
gccaaggtct ttgacttcgc cctctactac aagatggatg aggcctttga caacaaaaac     780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc     840
```

```
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtatccagcc     900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
tggctcaaca aggataagct caagaacctc atctggatac atgacaacct cgccggagga    1020
agcactgaca tcgtttacta cgacaacgac gagctgatat tcgtgagaaa cggctacgga    1080
agcaagccgg gactgataac atacatcaac ctcgcctcaa gcaaagccgg aaggtgggtt    1140
tatgtgccga agttcgcggg cgcgtgcatc cacgagtata ctggtaacct cggaggctgg    1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct    1260
gccaacgggc agtatggcta ctccgtgtgg agctactgcg gggtgggctg a             1311

<210> 72
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated polypeptide

<400> 72
Met Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
        115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
    130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
```

```
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
                325                 330                 335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
            340                 345                 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Ala Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
    370                 375                 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385                 390                 395                 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                 410                 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
            420                 425                 430
Cys Gly Val Gly
        435
```

<210> 73
<211> 1299
<212> DNA
<213> Environmental

<400> 73

```
atggctctgg aagagggcgg gcttataatg caggccttct actgggacgt cccaggtgga      60
ggaatctggt gggacaccat agcccagaag atacccgact gggcgagcgc cgggatttcg     120
gcaatatgga ttcctcccgc gagtaagggc atgagcggcg gctattcgat gggctacgac     180
ccctacgatt tcttcgacct cggtgagtac taccagaagg gaagcgttga gacccgcttc     240
ggatcaaaag aggagcttgt gaacatgata aacaccgccc atgctcacaa catgaaggtc     300
atagcggaca tagtcatcaa ccaccgcgcc ggcggcgacc tggagtggaa tcctttcacc     360
aacagctaca cctggaccga tttctcgaag gtcgcgtcgg gcaagtacac ggccaactac     420
ctcgacttcc acccgaacga gcttcacgcg ggcgattccg gaacatttgg aggctatccc     480
gacatatgcc acgacaagag ctgggaccag cactggctct gggccagcaa cgaaagctac     540
gccgcctacc tccggagcat cggcatcgac gcctggcgct tcgactacgt caagggctac     600
gctccctggg tcgttaagaa ctggctgaac cggtggggcg gctgggcggt tggagagtac     660
tgggacacca acgtcgatgc actcctgagc tgggcctacg acagcggtgc taaagtcttc     720
gacttcccgc tctactacaa gatggacgag gccttcgata acaacaacat ccccgccctc     780
gtggacgccc tcaagaacgg aggcacggtc gtcagccgcg acccgttcaa agccgtgacc     840
ttcgttgcca accacgatac caacataatc tggaacaagt atccggccta cgccttcatc     900
ctcacctatg agggacagcc ggcaatattc taccgcgact acgaggagtg gctcaacaag     960
gacaggctca ggaacctcat ctggatacac gaccacctcg cgggaggaag cacagacatc    1020
atctactacg acagcgacga gcttatcttc gtgagaaacg gctacgggga caagccggga    1080
ctgataacct acatcaacct cggctcaagc aaggccggaa ggtgggtcta cgttccgaag    1140
ttcgcaggct cgtgcataca cgagtacacc ggcaacctcg gcggctggat tgacaagtgg    1200
gttgactcaa gcggtcgggt ctaccttgag gcccccgccc acgacccggc caacggccag    1260
tacggctact ccgtatggag ctactgcggt gttgggtga                           1299
```

<210> 74
<211> 432
<212> PRT
<213> Environmental

<400> 74

```
Met Ala Leu Glu Glu Gly Gly Leu Ile Met Gln Ala Phe Tyr Trp Asp
 1               5                  10                  15
Val Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Ala Gln Lys Ile Pro
            20                  25                  30
```

```
Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser
        35                  40                  45
Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe
    50                  55                  60
Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Ser Val Glu Thr Arg Phe
65                  70                  75                  80
Gly Ser Lys Glu Glu Leu Val Asn Met Ile Asn Thr Ala His Ala His
                85                  90                  95
Asn Met Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly
            100                 105                 110
Asp Leu Glu Trp Asn Pro Phe Thr Asn Ser Tyr Thr Trp Thr Asp Phe
        115                 120                 125
Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His
    130                 135                 140
Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly Gly Tyr Pro
145                 150                 155                 160
Asp Ile Cys His Asp Lys Ser Trp Asp Gln His Trp Leu Trp Ala Ser
                165                 170                 175
Asn Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile Asp Ala Trp
            180                 185                 190
Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val Val Lys Asn Trp
        195                 200                 205
Leu Asn Arg Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn
    210                 215                 220
Val Asp Ala Leu Leu Ser Trp Ala Tyr Asp Ser Gly Ala Lys Val Phe
225                 230                 235                 240
Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Asn Asn
                245                 250                 255
Ile Pro Ala Leu Val Asp Ala Leu Lys Asn Gly Gly Thr Val Val Ser
            260                 265                 270
Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asn
        275                 280                 285
Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu
    290                 295                 300
Gly Gln Pro Ala Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys
305                 310                 315                 320
Asp Arg Leu Arg Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly
                325                 330                 335
Ser Thr Asp Ile Ile Tyr Tyr Asp Ser Asp Glu Leu Ile Phe Val Arg
            340                 345                 350
Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly
        355                 360                 365
Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ser
    370                 375                 380
Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Ile Asp Lys Trp
385                 390                 395                 400
Val Asp Ser Ser Gly Arg Val Tyr Leu Glu Ala Pro Ala His Asp Pro
                405                 410                 415
Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
            420                 425                 430
```

<210> 75
<211> 1299
<212> DNA
<213> Environmental

<400> 75

```
atggctctgg aagagggcgg gcttataatg caggcattct actgggacgt ccccatggga      60
ggaatctggt gggacacgat agcccagaag atacccgact gggcaagcgc cgggatttcg     120
gcgatatgga ttccccccgc gagcaagggt atgagcggcg gctattcgat gggctacgac     180
ccctacgatt attttgacct cggtgagtac taccagaagg gaacggtgga aacaagattc     240
ggctcaaagc aggagctcat aaacatgata aacaccgccc acgcctatgg catgaaggta     300
atagccgata tagtcatcaa ccaccgcgcc ggcggcgatc tggagtggaa ccccttcgtg     360
aacgactata cctggaccga cttctcgaag gtcgcgtcgg gtaaatacac ggccaactac     420
ctcgacttcc acccgaacga gctccacgcg ggcgattccg gaacatttgg aggctatccc     480
gacatatgcc acgacaagag ctgggaccag tactggctct gggccagcca ggagagctac     540
gcggcctatc tcaggagcat cggcatcgac gcctggcgct tcgactacgt caagggctat     600
gctccctggg tcgtcaggga ctggctgaac tggtggggag gctgggcagt tggagagtac     660
tgggacacca acgtcgacgc tgttctcaac tgggcatact cgagcggtgc caaggtcttt     720
gacttcgccc tctactacaa gatggacgag gccttcgata acaacaacat tcccgccctg     780
gtggacgccc tcagatacgg ccagacagtg gtcagccgcg acccgttcaa ggctgtgacg     840
tttgtagcca accacgatac cgacataatc tggaacaagt atccagccta cgcgttcatc     900
ctcacctacg agggccagcc gacaatattc taccgcgact acgaggagtg gctcaacaag     960
gacaagctca agaacctcat ctggatacat gacaacctcg ccggagggag cactgacatc    1020
gtttactacg acaacgacga gctgatattc gtgagaaacg gctacggaag caagccggga    1080
ctgataacat acatcaacct cggctcaagc aaagccggaa ggtgggttta cgttccgaag    1140
ttcgcaggct cgtgcataca cgagtacacc ggcaacctcg gcggctgggt ggacaagtgg    1200
gtggactcaa gcggctgggt ttacctcgag gctcctgccc acgacccggc caacggccag    1260
tacggctact ccgtttggag ctattgcggt gttgggtga                           1299
```

<210> 76
<211> 432
<212> PRT
<213> Environmental

<400> 76

```
Met Ala Leu Glu Glu Gly Gly Leu Ile Met Gln Ala Phe Tyr Trp Asp
 1               5                  10                  15
Val Pro Met Gly Gly Ile Trp Trp Asp Thr Ile Ala Gln Lys Ile Pro
            20                  25                  30
Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser
        35                  40                  45
Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Tyr
    50                  55                  60
Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe
65                  70                  75                  80
Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr
                85                  90                  95
Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly
            100                 105                 110
Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr Trp Thr Asp Phe
        115                 120                 125
Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His
    130                 135                 140
Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly Gly Tyr Pro
145                 150                 155                 160
Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser
                165                 170                 175
Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile Asp Ala Trp
            180                 185                 190
Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val Val Arg Asp Trp
        195                 200                 205
Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn
    210                 215                 220
```

```
Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe
225                 230                 235                 240
Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Asn Asn
                245                 250                 255
Ile Pro Ala Leu Val Asp Ala Leu Arg Tyr Gly Gln Thr Val Val Ser
            260                 265                 270
Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp
        275                 280                 285
Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu
    290                 295                 300
Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys
305                 310                 315                 320
Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu Ala Gly Gly
                325                 330                 335
Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Val Arg
            340                 345                 350
Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly
        355                 360                 365
Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ser
    370                 375                 380
Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Trp
385                 390                 395                 400
Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala His Asp Pro
                405                 410                 415
Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
            420                 425                 430
```

<210> 77
<211> 1299
<212> DNA
<213> Environmental

<400> 77

```
atggctctgg aagagggcgg gctcataatg caggccttct actgggacgt ccccatggga      60
ggaatctggt gggacacgat agcccagaag atacccgact gggcaagcgc cgggatttcg     120
gcgatatgga tccctcccgc gagcaagggt atgagcggcg gctattcgat gggctacgac     180
ccctacgatt attttgacct cggtgagtac taccagaagg gaacggtgga aacgaggttc     240
ggctcaaagc aggagctcat aaacatgata aacaccgccc acgcctatgg catgaaggta     300
atagccgata tagtcatcaa ccaccgcgcc ggcggtgacc tggagtggaa ccccttcgtg     360
aacgactata cctggaccga cttctcaaag gtcgcgtcgg gtaaatacac ggccaactac     420
ctcgacttcc acccgaacga gctccatgcg ggcgattccg gaacatttgg aggctatccc     480
gacatatgcc acgacaagag ctgggaccag tactggctct gggccagcca ggagagctac     540
gcggcatatc tcaggagcat cggcatcgat gcctggcgct tcgactacgt caagggctat     600
gctccctggg tcgtcaagga ctggctgaac tggtggggag gctgggcggt tggagagtac     660
tgggacacca acgtcgacgc tgttctcaac tgggcatact cgagcggtgc caaggtcttt     720
gacttcgccc tctactacaa gatggacgag gccttcgata acaacaacat tcccgccctg     780
gtggacgccc tcagatacgg tcagacagtg gtcagccgcg acccgttcaa ggctgtgacg     840
tttgtagcca accacgatac cgacataatc tggaacaagt atccagccta cgcgttcatc     900
ctcacctacg agggccagcc gacaatattc taccgcgact acgaggagtg gctcaacaag     960
gataagctca agaacctcat ctggatacat gacaacctcg ccggagggag cactgacatc    1020
gtttactacg acaacgacga gctgatattc gtgagaaacg gctacggaag caagccggga    1080
ctgataacat acatcaacct cgcctcaagc aaagccggaa ggtgggttta cgttccgaag    1140
ttcgcaggct cgtgcataca cgagtacacc ggcaatctcg gcggctgggt ggacaagtgg    1200
gtggactcaa gcggctgggt ctacctcgag gctcctgccc acgacccggc caacggccag    1260
tacggctact ccgtctggag ctactgcggt gttgggtga                           1299
```

<210> 78

<211> 432
<212> PRT
<213> Environmental

<400> 78

```
Met Ala Leu Glu Glu Gly Gly Leu Ile Met Gln Ala Phe Tyr Trp Asp
 1               5                  10                  15
Val Pro Met Gly Gly Ile Trp Trp Asp Thr Ile Ala Gln Lys Ile Pro
            20                  25                  30
Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser
        35                  40                  45
Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Tyr
    50                  55                  60
Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe
65                  70                  75                  80
Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr
                85                  90                  95
Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly
            100                 105                 110
Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr Trp Thr Asp Phe
        115                 120                 125
Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His
    130                 135                 140
Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly Gly Tyr Pro
145                 150                 155                 160
Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser
                165                 170                 175
Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile Asp Ala Trp
            180                 185                 190
Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val Val Lys Asp Trp
        195                 200                 205
Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn
    210                 215                 220
Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe
225                 230                 235                 240
Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Asn Asn
                245                 250                 255
Ile Pro Ala Leu Val Asp Ala Leu Arg Tyr Gly Gln Thr Val Val Ser
            260                 265                 270
Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp
        275                 280                 285
Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu
    290                 295                 300
Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys
305                 310                 315                 320
Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu Ala Gly Gly
                325                 330                 335
Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Val Arg
            340                 345                 350
Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Ala
        355                 360                 365
Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ser
    370                 375                 380
Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Trp
385                 390                 395                 400
Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala His Asp Pro
                405                 410                 415
```

```
Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
            420                 425                 430

<210> 79
<211> 1386
<212> DNA
<213> Bacterial

<400> 79
atgaagcctg cgaaactcct cgtctttgtg ctcgtagtct ctatcctcgc ggggctctac      60
gcccagcccg cgggggcggc caagtacctg gagctcgaag agggcggcgt cataatgcag     120
gcgttctact gggacgtgcc ttcaggagga atatggtggg acacaatacg gcagaagata     180
ccggagtggt acgatgccgg aatctccgca atatggattc ccccggcgag caagggcatg     240
ggcggcgcct attcgatggg ctacgacccc tacgacttct ttgacctcgg tgagtacgac     300
cagaagggaa cggtagagac gcgctttggc tccaagcagg agctcgtgaa catgataaac     360
accgcccacg cctacggcat caaggtcatc gcagacatag taatcaacca ccgcgccgga     420
ggagaccttg agtggaaccc cttcgtcaat gactacacct ggacggactt ctcgaaggtc     480
gcttccggca agtacacggc caactacctc gacttccacc ccaacgaggt caagtgctgc     540
gacgagggca cctttggagg gttcccggac atagcccacg agaagagctg ggaccagtac     600
tggctctggg cgagcaacga gagctacgcc gcctacctca ggagcatcgg cgttgacgca     660
tggcgcttcg actacgtcaa gggctacgga gcgtgggtcg tcaaggactg gctggactgg     720
tggggaggct gggccgtcgg ggagtactgg gacacaaacg ttgatgcact gctcaactgg     780
gcctactcga gcgatgcaaa agtcttcgac ttcccgctct actacaagat ggacgcggcc     840
tttgacaaca agaacattcc cgcactcgtc gaggccctca agaacggggg cacagtcgtc     900
agccgcgacc cgtttaaggc cgtaaccttc gttgcaaacc acgacacgga cataatttgg     960
aacaagtacc cggcctacgc cttcatcctc acctacgagg gccagccgac gatattctac    1020
cgcgactacg aggagtggct caacaaggac aggctcaaga acctcatctg gatacacgac    1080
cacctcgccg gtggaagcac cgacatagtc tactacgata acgatgaact catcttcgtc    1140
aggaacggct acggggacaa gccggggctt ataacctaca tcaacctagg ctcgagcaag    1200
gccgggaggt gggtctacgt tccgaagttc gcgggagcgt gcatccacga gtacaccggc    1260
aacctcggcg gctgggtgga caagtgggtg gactcaagcg ggtgggtgta cctcgaggcc    1320
cctgcccacg acccggccaa cggctattac ggctactccg tctggagcta ctgcggggtg    1380
ggctga                                                               1386

<210> 80
<211> 461
<212> PRT
<213> Bacterial

<400> 80
Met Lys Pro Ala Lys Leu Leu Val Phe Val Leu Val Val Ser Ile Leu
 1               5                  10                  15
Ala Gly Leu Tyr Ala Gln Pro Ala Gly Ala Ala Lys Tyr Leu Glu Leu
            20                  25                  30
Glu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Ser
        35                  40                  45
Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln Lys Ile Pro Glu Trp Tyr
    50                  55                  60
Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met
65                  70                  75                  80
Gly Gly Ala Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu
                85                  90                  95
Gly Glu Tyr Asp Gln Lys Gly Thr Val Glu Thr Arg Phe Gly Ser Lys
            100                 105                 110
Gln Glu Leu Val Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys
        115                 120                 125
Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp Leu Glu
```

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    130                 135                 140
Trp Asn Pro Phe Val Asn Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val
145                 150                 155                 160
Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu
                165                 170                 175
Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala
            180                 185                 190
His Glu Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser Asn Glu Ser
        195                 200                 205
Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp
    210                 215                 220
Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asp Trp
225                 230                 235                 240
Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala
                245                 250                 255
Leu Leu Asn Trp Ala Tyr Ser Ser Asp Ala Lys Val Phe Asp Phe Pro
            260                 265                 270
Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp Asn Lys Asn Ile Pro Ala
        275                 280                 285
Leu Val Glu Ala Leu Lys Asn Gly Gly Thr Val Val Ser Arg Asp Pro
    290                 295                 300
Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp
305                 310                 315                 320
Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro
                325                 330                 335
Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu
            340                 345                 350
Lys Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Asp
        355                 360                 365
Ile Val Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Val Arg Asn Gly Tyr
    370                 375                 380
Gly Asp Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys
385                 390                 395                 400
Ala Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His
                405                 410                 415
Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Trp Val Asp Ser
            420                 425                 430
Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala His Asp Pro Ala Asn Gly
        435                 440                 445
Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
    450                 455                 460
```

<210> 81
<211> 1386
<212> DNA
<213> Bacterial

<400> 81

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atgaagaagt ttgtcgccct gttcataacc atgtttttcg tagtgagcat ggcagtcgtt      60
gcacagccag ctagcgccgc aaagtattcc gagctcgaag aaggcggcgt tataatgcag     120
gccttctact gggacgtccc aggtggagga atctggtggg acaccatcag gagcaagata     180
ccggagtggt acgaggcggg aatatccgcc atttggattc cgccagccag caaggggatg     240
agcggcggtt actcgatggg ctacgatccc tacgatttct ttgacctcgg cgagtacaac     300
cagaagggaa ccatcgaaac gcgctttggc tctaaacagg agctcatcaa tatgataaac     360
acggcccatg cctacggcat aaaggtcata gcggacatcg tcataaacca ccgcgcaggc     420
ggagacctcg agtggaaccc gttcgttggg gactacacct ggacggactt ctcaaaggtg     480
gcctcgggca aatatactgc caactacctc gacttccacc ccaacgaggt caagtgctgt     540
```

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gacgagggca catttggagg cttcccagac atagcccacg agaagagctg ggaccagcac     600
tggctctggg cgagcgatga gagctacgcc gcctacctaa ggagcatcgg cgttgatgcc     660
tggcgctttg actacgtgaa gggctacgga gcgtgggtcg tcaaggactg gctcaactgg     720
tggggcggct gggccgttgg cgagtactgg gacaccaacg ttgatgcact cctcaactgg     780
gcctactcga gcggcgccaa ggtcttcgac ttcccgctct actacaagat ggatgaggcc     840
tttgacaaca aaaacattcc agcgctcgtc tctgcccttc agaacggcca gactgttgtc     900
tcccgcgacc cgttcaaggc cgtaaccttt gtagcaaacc acgacaccga tataatctgg     960
aacaagtacc ttgcttatgc tttcatcctc acctacgaag gccagcccgt catattctac    1020
cgcgactacg aggagtggct caacaaggac aggttgaaca acctcatatg gatacacgac    1080
cacctcgcag gtggaagcac gagcatagtc tactacgaca gcgacgagat gatcttcgtg    1140
aggaacggct atggaagcaa gcctggcctt ataacttaca tcaacctcgg ctcgagcaag    1200
gttggaaggt gggtttatgt gccgaagttc gcgggcgcgt gcatccacga gtatactggt    1260
aacctcggag gctgggtaga caagtacgtc tactcaagcg gctgggtcta tctcgaagct    1320
ccagcttacg accctgccaa cgggcagtat ggctactccg tgtggagcta ttgcggtgtt    1380
gggtga                                                              1386

<210> 82
<211> 461
<212> PRT
<213> Bacterial

<400> 82
Met Lys Lys Phe Val Ala Leu Phe Ile Thr Met Phe Phe Val Val Ser
 1               5                  10                  15
Met Ala Val Val Ala Gln Pro Ala Ser Ala Ala Lys Tyr Ser Glu Leu
            20                  25                  30
Glu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Gly
        35                  40                  45
Gly Gly Ile Trp Trp Asp Thr Ile Arg Ser Lys Ile Pro Glu Trp Tyr
    50                  55                  60
Glu Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met
65                  70                  75                  80
Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu
                85                  90                  95
Gly Glu Tyr Asn Gln Lys Gly Thr Ile Glu Thr Arg Phe Gly Ser Lys
            100                 105                 110
Gln Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys
        115                 120                 125
Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp Leu Glu
    130                 135                 140
Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val
145                 150                 155                 160
Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu
                165                 170                 175
Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala
            180                 185                 190
His Glu Lys Ser Trp Asp Gln His Trp Leu Trp Ala Ser Asp Glu Ser
        195                 200                 205
Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp
    210                 215                 220
Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asn Trp
225                 230                 235                 240
Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala
                245                 250                 255
Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe Asp Phe Pro
            260                 265                 270
Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Lys Asn Ile Pro Ala
```

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        275                 280                 285
Leu Val Ser Ala Leu Gln Asn Gly Gln Thr Val Val Ser Arg Asp Pro
    290                 295                 300
Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp
305                 310                 315                 320
Asn Lys Tyr Leu Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro
                325                 330                 335
Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu
            340                 345                 350
Asn Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Ser
        355                 360                 365
Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile Phe Val Arg Asn Gly Tyr
    370                 375                 380
Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys
385                 390                 395                 400
Val Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His
                405                 410                 415
Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Tyr Val Tyr Ser
            420                 425                 430
Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala Tyr Asp Pro Ala Asn Gly
        435                 440                 445
Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
    450                 455                 460
```

<210> 83
<211> 1299
<212> DNA
<213> Environmental

<400> 83

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atggctctgg aagacggcgg gctcataatg caggccttct actgggatgt tcctggagga      60
ggaatctggt gggacacaat agctcaaaag atacccgaat gggcaagtgc aggaatctca     120
gcgatatgga ttccaccagc gagtaagggc atgagcggtg gttattccat gggctacgat     180
ccctacgatt tctttgacct cggcgagtac tatcagaagg ggacagttga gacgcgcttc     240
ggctcaaagg aagaactggt gaacatgata aacaccgcac actcctacgg cataaaggtg     300
atagcagaca tagtcataaa ccaccgcgcc ggtggagacc ttgagtggaa ccccttcgtg     360
aacgactata cctggacaga cttctcaaaa gtcgcctccg gtaaatatac ggccaactac     420
cttgacttcc acccaaacga gcttcactgt tgtgatgaag gtacctttgg aggataccct     480
gatatatgtc acgacaaaag ctgggaccag tactggctct gggcgagcag cgaaagctac     540
gctgcctacc tcaggagcat aggggttgac gcctggcgtt tcgactacgt caagggctac     600
ggagcatggg ttgttaacga ctggctcagc tggtggggag gctgggccgt tggagagtac     660
tgggacacga acgttgatgc actcctcaac tgggcataca gcagcggcgc caaggtcttt     720
gacttcccgc tctactacaa gatggacgaa gccttcgaca acaccaacat cccggcatta     780
gtggatgcac tcagatacgg ccagacagtg gtcagccgcg atcccttcaa ggcggtaact     840
ttcgttgcca accacgatac agatataatc tggaacaagt atccggctta tgcattcatc     900
cttacctatg agggacagcc tgttatattc taccgcgact acgaggagtg gctcaacaag     960
gataagctta acaacctcat ctggatacac gatcaccttg ctggagggag tactgacatt    1020
gtttactacg acagcgacga gcttatcttt gtgagaaacg gctatggcac caaaccagga    1080
ctgataacct atatcaacct cggctcaagc aaagttggaa ggtgggtcta cgttccaaag    1140
ttcgccggtt catgcatcca cgagtacacc ggcaacctcg gcggttggat agacaagtac    1200
gtctcctcca gcggctgggt ctatcttgag gccccagccc acgacccggc gaacggctac    1260
tacggctact ccgtatggag ctactgcggg gttgggtga                           1299
```

<210> 84
<211> 432
<212> PRT
<213> Environmental

<400> 84

```
Met Ala Leu Glu Asp Gly Gly Leu Ile Met Gln Ala Phe Tyr Trp Asp
 1               5                  10                  15
Val Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Ala Gln Lys Ile Pro
            20                  25                  30
Glu Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser
        35                  40                  45
Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe
    50                  55                  60
Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe
65                  70                  75                  80
Gly Ser Lys Glu Glu Leu Val Asn Met Ile Asn Thr Ala His Ser Tyr
                85                  90                  95
Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly
            100                 105                 110
Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr Trp Thr Asp Phe
        115                 120                 125
Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His
    130                 135                 140
Pro Asn Glu Leu His Cys Cys Asp Glu Gly Thr Phe Gly Gly Tyr Pro
145                 150                 155                 160
Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser
                165                 170                 175
Ser Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp
            180                 185                 190
Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Asn Asp Trp
        195                 200                 205
Leu Ser Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn
    210                 215                 220
Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe
225                 230                 235                 240
Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Thr Asn
                245                 250                 255
Ile Pro Ala Leu Val Asp Ala Leu Arg Tyr Gly Gln Thr Val Val Ser
            260                 265                 270
Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp
        275                 280                 285
Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu
    290                 295                 300
Gly Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys
305                 310                 315                 320
Asp Lys Leu Asn Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly
                325                 330                 335
Ser Thr Asp Ile Val Tyr Tyr Asp Ser Asp Glu Leu Ile Phe Val Arg
            340                 345                 350
Asn Gly Tyr Gly Thr Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly
        355                 360                 365
Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ser
    370                 375                 380
Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Ile Asp Lys Tyr
385                 390                 395                 400
Val Ser Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala His Asp Pro
                405                 410                 415
Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
            420                 425                 430
```

<210> 85
<211> 1299
<212> DNA
<213> Environmental

<400> 85
atggctctgg aagagggcgg gcttataatg caggcattct attgggacgt cccaggtgga 60
ggaatctggt gggacaccat agcccagaag atacccgaat gggcaagtgc aggaatctca 120
gcgatatgga ttccaccagc gagtaaggga atgagcggtg gttattccat gggctacgat 180
ccctacgatt tctttgacct cggcgagtac tatcagaagg ggacagttga gacgcgcttc 240
ggctcaaagg aagaactggt gaacatgata aacaccgcac actcctacgg cataaaggtg 300
atagcggaca tagtcataaa ccaccgcgcc ggtggaggcc tcgagtggaa ccccttcgtg 360
aacgactata cctggacaga cttctcaaaa gtcgcctccg gtaaatatac agccaactac 420
cttgacttcc acccaaacga gcttcactgt tgtgatgaag gtacctttgg aggataccct 480
gatatatgtc acgacaaaag ctgggaccag tactggctct gggcgagcag cgaaagctac 540
gctgcctacc tcaggagcat aggggttgac gcctggtgtt tcgactacgt caagggctac 600
ggagcctggg ttgttaacga ctggctcagc tggtggggag gctgggccgt tggagagtac 660
tgggacacta acgttgatgc actcctcaac tgggcataca acagcggcgc caaggtcttt 720
gacttcccgc tctactacaa gatggacgaa gccttcgaca ataccaacat ccccgctttg 780
gtttacgccc tcaagaatgg cgggacagtg gtcagccgcg acccattcaa ggcggtaact 840
ttcgttgcca accacgatac agatataatc tggaacaagt atccggctta tgcattcatc 900
cttacctatg agggacagcc tgttatattc taccgcgact acgaggagtg gctcaacaag 960
gataagctta acaacctcat ctggatacac gatcaccttg ctggagggag tactgacatt 1020
gtttactacg acagcgacga gcttatcttt gtgagaaacg gctatggcac caaaccagga 1080
ctgataacct atatcaacct cggctcaagc aaagctggaa ggtgggtcta cgttccaaag 1140
ttcgccggtt catgcatcca cgagtacacc ggcagcctcg gcggttggat agacaagtac 1200
gtctcctcca gcggctgggt ctaccttgag gccccggccc acgacccggc caatggccag 1260
tatggctact ccgtctggag ctattgcggg gttgggtga 1299

<210> 86
<211> 432
<212> PRT
<213> Environmental

<400> 86
Met Ala Leu Glu Glu Gly Gly Leu Ile Met Gln Ala Phe Tyr Trp Asp
1 5 10 15
Val Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Ala Gln Lys Ile Pro
20 25 30
Glu Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser
35 40 45
Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe
50 55 60
Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe
65 70 75 80
Gly Ser Lys Glu Glu Leu Val Asn Met Ile Asn Thr Ala His Ser Tyr
85 90 95
Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly
100 105 110
Gly Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr Trp Thr Asp Phe
115 120 125
Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His
130 135 140
Pro Asn Glu Leu His Cys Cys Asp Glu Gly Thr Phe Gly Gly Tyr Pro
145 150 155 160
Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser
165 170 175

```
Ser Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp
            180                 185                 190
Cys Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Asn Asp Trp
        195                 200                 205
Leu Ser Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn
    210                 215                 220
Val Asp Ala Leu Leu Asn Trp Ala Tyr Asn Ser Gly Ala Lys Val Phe
225                 230                 235                 240
Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Thr Asn
                245                 250                 255
Ile Pro Ala Leu Val Tyr Ala Leu Lys Asn Gly Gly Thr Val Val Ser
            260                 265                 270
Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp
        275                 280                 285
Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu
    290                 295                 300
Gly Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys
305                 310                 315                 320
Asp Lys Leu Asn Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly
                325                 330                 335
Ser Thr Asp Ile Val Tyr Tyr Asp Ser Asp Glu Leu Ile Phe Val Arg
            340                 345                 350
Asn Gly Tyr Gly Thr Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly
        355                 360                 365
Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ser
    370                 375                 380
Cys Ile His Glu Tyr Thr Gly Ser Leu Gly Gly Trp Ile Asp Lys Tyr
385                 390                 395                 400
Val Ser Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala His Asp Pro
                405                 410                 415
Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
            420                 425                 430
```

<210> 87
<211> 1419
<212> DNA
<213> Environmental

<400> 87

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atgttcctgc tcgcgttttt gctcactgcc tcgctgttct gcccaacagg acagcccgcc      60
aaggctgccg caccgtttaa cggcaccatg atgcagtatt ttgaatggta cttgccggat     120
gatggcacgt tatggaccaa agtggccaat gaagccaaca acttatccag ccttggcatc     180
accgctcttt ggctgccgcc cgcttacaaa ggaacaagcc gcagcgacgt agggtacgga     240
gtatacgact tgtatgacct cggcgaattc aatcaaaaag ggaccgtccg cacaaaatac     300
ggaacaaaag ctcaatatct tcaagccatt caagccgccc acgccgctgg aatgcaagtg     360
tacgccgatg tcgtgttcga ccataaaggc ggcgctgacg gcacggaatg ggtggacgcc     420
gtcgaagtca atccgtccga ccgcaaccaa gaaatctcgg gcacctatca aatccaagca     480
tggacgaaat ttgattttcc cgggcggggc aacacctact ccagctttaa gtggcgctgg     540
taccattttg acggcgttga ttgggacgaa agccgaaaat tgagccgcat ttacaaattc     600
cgcggcatcg gcaaagcgtg ggattgggaa gtagacacgg aaaacggaaa ctatgactac     660
ttaatgtatg ccgaccttga tatggatcat cccgaagtcg tgaccgagct gaaaaactgg     720
gggaaatggt atgtcaacac aacgaacatt gatgggttcc ggcttgatgc cgtcaagcat     780
attaagttca gttttttttcc tgattggttg tcgtatgtgc gttctcagac tggcaagccg     840
ctatttaccg tcggggaata ttggagctat gacatcaaca agttgcacaa ttacattacg     900
aaaacagacg gaacgatgtc tttgtttgat gccccgttac acaacaaatt ttataccgct     960
tccaaatcag ggggcgcatt tgatatgcgc acgttaatga ccaatactct catgaaagat    1020
caaccgacat tggccgtcac cttcgttgat aatcatgaca ccgaacccgg ccaagcgctg    1080
```

```
cagtcatggg tcgacccatg gttcaaaccg ttggcttacg cctttattct aactcggcag    1140
gaaggatacc cgtgcgtctt ttatggtgac tattatggca ttccacaata taacattcct    1200
tcgctgaaaa gcaaaatcga tccgctcctc atcgcgcgca gggattatgc ttacggaacg    1260
caacatgatt atcttgatca ctccgacatc atcgggtgga caagggaagg ggtcactgaa    1320
aaaccaggat ccgggctggc cgcactgatc accgatgggc cgggaggaag caaatggatg    1380
tactgttggc aaacaacacg ctggaaaagt gttctatga                           1419

<210> 88
<211> 472
<212> PRT
<213> Environmental

<400> 88
Met Phe Leu Leu Ala Phe Leu Leu Thr Ala Ser Leu Phe Cys Pro Thr
 1               5                  10                  15
Gly Gln Pro Ala Lys Ala Ala Ala Pro Phe Asn Gly Thr Met Met Gln
            20                  25                  30
Tyr Phe Glu Trp Tyr Leu Pro Asp Asp Gly Thr Leu Trp Thr Lys Val
        35                  40                  45
Ala Asn Glu Ala Asn Asn Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp
    50                  55                  60
Leu Pro Pro Ala Tyr Lys Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly
65                  70                  75                  80
Val Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val
                85                  90                  95
Arg Thr Lys Tyr Gly Thr Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala
            100                 105                 110
Ala His Ala Ala Gly Met Gln Val Tyr Ala Asp Val Val Phe Asp His
        115                 120                 125
Lys Gly Gly Ala Asp Gly Thr Glu Trp Val Asp Ala Val Glu Val Asn
    130                 135                 140
Pro Ser Asp Arg Asn Gln Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala
145                 150                 155                 160
Trp Thr Lys Phe Asp Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe
                165                 170                 175
Lys Trp Arg Trp Tyr His Phe Asp Gly Val Asp Trp Asp Glu Ser Arg
            180                 185                 190
Lys Leu Ser Arg Ile Tyr Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp
        195                 200                 205
Trp Glu Val Asp Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala
    210                 215                 220
Asp Leu Asp Met Asp His Pro Glu Val Val Thr Glu Leu Lys Asn Trp
225                 230                 235                 240
Gly Lys Trp Tyr Val Asn Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp
                245                 250                 255
Ala Val Lys His Ile Lys Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr
            260                 265                 270
Val Arg Ser Gln Thr Gly Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp
        275                 280                 285
Ser Tyr Asp Ile Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asp Gly
    290                 295                 300
Thr Met Ser Leu Phe Asp Ala Pro Leu His Asn Lys Phe Tyr Thr Ala
305                 310                 315                 320
Ser Lys Ser Gly Gly Ala Phe Asp Met Arg Thr Leu Met Thr Asn Thr
                325                 330                 335
Leu Met Lys Asp Gln Pro Thr Leu Ala Val Thr Phe Val Asp Asn His
            340                 345                 350
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Asp Thr Glu Pro Gly Gln Ala Leu Gln Ser Trp Val Asp Pro Trp Phe
        355                 360                 365
Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro
    370                 375                 380
Cys Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro
385                 390                 395                 400
Ser Leu Lys Ser Lys Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr
                405                 410                 415
Ala Tyr Gly Thr Gln His Asp Tyr Leu Asp His Ser Asp Ile Ile Gly
            420                 425                 430
Trp Thr Arg Glu Gly Val Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala
        435                 440                 445
Leu Ile Thr Asp Gly Pro Gly Gly Ser Lys Trp Met Tyr Cys Trp Gln
    450                 455                 460
Thr Thr Arg Trp Lys Ser Val Leu
465                 470
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<210> 89
<211> 3301
<212> DNA
<213> Bacterial

<400> 89

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gatttgcccg ataatccgcg cctgaaaggg acgagcggct acgatggcga cggtgaatgg     180
tcgaatgact ttttcggcgg agacatcgcc ggaattgaac aaaagttgga ttatttgcag     240
tcgcttggag tgaacacgat ttacttaaat ccgatcgcca atgcgccatc gaaccataaa     300
tatgatgcga gcaattacaa agaattggat ccgatgttcg gttccccgga agaattccaa     360
tcgtttgtgc aggcgcttgc gaaccggggg atgcatctca tcttagacgg ggtgttcaac     420
cacgtatccg acgattcgat ttactttgac cgctaccacc gctatccgac cgtcggtgcg     480
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tttcatcttt ggttcaatat tgaaaacaaa aaagtcaatg gccattatca ataccaatca     660
tggtggggct atgacagtct gccggagttt aagtcggtga cgggggaaaa agtgccgcat     720
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gcgaaaagct ggattgccct cggcgcctcc ggctggcggt tggatgtggc caatgaggtg     840
gatccggcgt tttggcgcga gtttcgccaa gaattgcttc aagggtcgta cggccgcggt     900
ccgacgttaa aagaggggga gcagccgctc attttagggg aaatttggga tgacgcatcg     960
aaatattttc taggcgacca gtacgattcc gtgatgaact accggttccg cggggcggtg    1020
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gaagactacc caagtgaagc gttttatgcg ctgatgaact taatcggttc gcatgacacg    1140
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ccgaattata atgaggaact tgggaaaaag cggctcaagc tggcggtgat tttgcagatg    1260
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gcgctcattg ccatcaaccg cggcaatgag gacaagacgg tggcgcttga cgtcgcttcg    1560
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gtgacgttaa cgtgggaagg aaatgcatcg agataccgaa tttacgagtc cacgttaaaa    1800
ggtgccggtt atacgatggt gcaagagacg gaaacaactt cggccacgat cggttcgttg    1860
acgaacggaa cagcctatta ctttgccgtt gcggcggtcg atgaaaacgg gaatgaatca    1920
ccgaaggtcg aaacgaatcg cgtcgttcct cattacccgc tgacgagcga caatgtccag    1980
ttcgtgacaa cgttaagcga tgccacactg gatttgtcaa agccgcagca agtggatgtc    2040
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catgtcaaca tcgacaatgt gacaagcaaa ggagcagctg atgggttgca agcggtgttg    2100
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gacggcgacg ccaacgtgtt ccgagctgcc ttcactccgc tcgccgcagg gacgtatacg    2220
tatcgttatg cgctgacgac caaccttggc gaggagtgga tgtatacaga agagaagcaa    2280
gtgacgtttg cggcagacaa cagcgaccaa atagcgccag cagacgccat cgagctgcgg    2340
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ggggatgctt atttgttagc catcgagcgc aacggtgata tcgtgcatac aaccacttcg    2460
atcggcgatt catttacaga ctacgatgtc gaaaacggca ccgagtacac gtatgttgtc    2520
aagttgtatg accgcgccgg caatgttgtg gcgtcaaaca cggtcaaggt gacgccggac    2580
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cgaattacga ttccgaacag cttgaacggc tggaacacag gggcctggga gatgtcgcgc    2700
aacggtgcgg tgacgcccga ttggcaattt accgtcgagg tgcaggaagg ggaaacgatc    2760
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gcgaaaaaca caaaagatta cgtgctgaat ttagaaacga agcaattcaa aaagcttctc    3240
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a                                                                    3301
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<210> 90
<211> 1100
<212> PRT
<213> Bacterial

<400> 90

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Gly Asn Pro Ser Asn Asp Asn Ser Lys Gln Gln Ala Arg Gly Ala Gln
            20                  25                  30
Pro Ile Glu His Arg Asp Trp Ser Asp Leu Pro Asp Asn Pro Arg Leu
        35                  40                  45
Lys Gly Thr Ser Gly Tyr Asp Gly Asp Gly Glu Trp Ser Asn Asp Phe
    50                  55                  60
Phe Gly Gly Asp Ile Ala Gly Ile Glu Gln Lys Leu Asp Tyr Leu Gln
65                  70                  75                  80
Ser Leu Gly Val Asn Thr Ile Tyr Leu Asn Pro Ile Ala Asn Ala Pro
                85                  90                  95
Ser Asn His Lys Tyr Asp Ala Ser Asn Tyr Lys Glu Leu Asp Pro Met
            100                 105                 110
Phe Gly Ser Pro Glu Glu Phe Gln Ser Phe Val Gln Ala Leu Ala Asn
        115                 120                 125
Arg Gly Met His Leu Ile Leu Asp Gly Val Phe Asn His Val Ser Asp
    130                 135                 140
Asp Ser Ile Tyr Phe Asp Arg Tyr His Arg Tyr Pro Thr Val Gly Ala
145                 150                 155                 160
Tyr Glu Tyr Trp Glu Ala Val Tyr Asp Leu Met Asn Glu Lys Gly Leu
                165                 170                 175
Ser Glu Glu Glu Ala Arg Lys Gln Val Glu Glu Lys Phe Lys Gln Glu
            180                 185                 190
Gly Gln Thr Phe Ser Pro Tyr Gly Phe His Leu Trp Phe Asn Ile Glu
        195                 200                 205
Asn Lys Lys Val Asn Gly His Tyr Gln Tyr Gln Ser Trp Trp Gly Tyr
    210                 215                 220
```

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Asp Ser Leu Pro Glu Phe Lys Ser Val Thr Gly Glu Lys Val Pro His
225                 230                 235                 240
Pro Ser Glu Leu Asn Asn Asp Ala Leu Ala Asn Tyr Ile Phe Arg Glu
                245                 250                 255
Ser Asp Ser Val Ala Lys Ser Trp Ile Ala Leu Gly Ala Ser Gly Trp
            260                 265                 270
Arg Leu Asp Val Ala Asn Glu Val Asp Pro Ala Phe Trp Arg Glu Phe
        275                 280                 285
Arg Gln Glu Leu Leu Gln Gly Ser Tyr Gly Arg Gly Pro Thr Leu Lys
    290                 295                 300
Glu Gly Glu Gln Pro Leu Ile Leu Gly Glu Ile Trp Asp Asp Ala Ser
305                 310                 315                 320
Lys Tyr Phe Leu Gly Asp Gln Tyr Asp Ser Val Met Asn Tyr Arg Phe
                325                 330                 335
Arg Gly Ala Val Leu Asp Phe Leu Lys Asn Gly Asn Ala Glu Glu Ala
            340                 345                 350
Asp Lys Arg Leu Thr Ala Ile Arg Glu Asp Tyr Pro Ser Glu Ala Phe
        355                 360                 365
Tyr Ala Leu Met Asn Leu Ile Gly Ser His Asp Thr Ala Arg Ala Val
    370                 375                 380
Phe Leu Leu Gly Asn Gly Thr Asp Ser Ser Glu Arg Ala Glu Leu Asp
385                 390                 395                 400
Pro Asn Tyr Asn Glu Glu Leu Gly Lys Lys Arg Leu Lys Leu Ala Val
                405                 410                 415
Ile Leu Gln Met Gly Tyr Pro Gly Ala Pro Thr Ile Tyr Tyr Gly Asp
            420                 425                 430
Glu Ala Gly Val Thr Gly Ser Lys Asp Pro Asp Asn Arg Arg Thr Tyr
        435                 440                 445
Pro Trp Gly Lys Glu Asp Gln Asn Leu Leu Ser His Tyr Gln Lys Val
    450                 455                 460
Gly His Ile Arg Gln His His Gln Ser Leu Leu Ala His Gly Asp Ile
465                 470                 475                 480
Lys Thr Val Tyr Ala Gln Gly Asp Val Tyr Val Phe Ala Arg Gln Tyr
                485                 490                 495
Gly Arg Glu Ala Ala Leu Ile Ala Ile Asn Arg Gly Asn Glu Asp Lys
            500                 505                 510
Thr Val Ala Leu Asp Val Ala Ser Leu Leu Pro Asn Gly Thr Val Leu
        515                 520                 525
Thr Asp Glu Leu His Asp Gly Gly Glu Ala Thr Val Ala Gly Gly Thr
    530                 535                 540
Leu Thr Val Thr Ile Pro Ala Leu Asp Gly Arg Met Met Phe Gly Thr
545                 550                 555                 560
Val Thr Ala Glu Met Pro Ala Ala Val Ser Asn Leu Gln Ala Ser Ala
                565                 570                 575
Ser Asp Gly Cys Val Thr Leu Thr Trp Glu Gly Asn Ala Ser Arg Tyr
            580                 585                 590
Arg Ile Tyr Glu Ser Thr Leu Lys Gly Ala Gly Tyr Thr Met Val Gln
        595                 600                 605
Glu Thr Glu Thr Thr Ser Ala Thr Ile Gly Ser Leu Thr Asn Gly Thr
    610                 615                 620
Ala Tyr Tyr Phe Ala Val Ala Ala Val Asp Glu Asn Gly Asn Glu Ser
625                 630                 635                 640
Pro Lys Val Glu Thr Asn Arg Val Val Pro His Tyr Pro Leu Thr Ser
                645                 650                 655
Asp Asn Val Gln Phe Val Thr Thr Leu Ser Asp Ala Thr Leu Asp Leu
            660                 665                 670
Ser Lys Pro Gln Gln Val Asp Val His Val Asn Ile Asp Asn Val Thr
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675 680 685
Ser Lys Gly Ala Ala Asp Gly Leu Gln Ala Val Leu Gln Val Lys Gly
690 695 700
Pro His Asp Glu Thr Trp Lys Glu Tyr Arg Ala Ala Tyr Gln Gly Gln
705 710 715 720
Asp Gly Asp Ala Asn Val Phe Arg Ala Ala Phe Thr Pro Leu Ala Ala
725 730 735
Gly Thr Tyr Thr Tyr Arg Tyr Ala Leu Thr Thr Asn Leu Gly Glu Glu
740 745 750
Trp Met Tyr Thr Glu Glu Lys Gln Val Thr Phe Ala Ala Asp Asn Ser
755 760 765
Asp Gln Ile Ala Pro Ala Asp Ala Ile Glu Leu Arg Gln Pro Ala Val
770 775 780
Glu Ser Gly Gln Val Asn Leu Ser Trp Thr Phe Val Gly Lys Lys Asp
785 790 795 800
Gly Asp Ala Tyr Leu Leu Ala Ile Glu Arg Asn Gly Asp Ile Val His
805 810 815
Thr Thr Thr Ser Ile Gly Asp Ser Phe Thr Asp Tyr Asp Val Glu Asn
820 825 830
Gly Thr Glu Tyr Thr Tyr Val Val Lys Leu Tyr Asp Arg Ala Gly Asn
835 840 845
Val Val Ala Ser Asn Thr Val Lys Val Thr Pro Asp Ile Val Met Val
850 855 860
Lys Val Ile Phe Lys Val Arg Ala Pro Asp Tyr Thr Pro Leu Asp Ala
865 870 875 880
Arg Ile Thr Ile Pro Asn Ser Leu Asn Gly Trp Asn Thr Gly Ala Trp
885 890 895
Glu Met Ser Arg Asn Gly Ala Val Thr Pro Asp Trp Gln Phe Thr Val
900 905 910
Glu Val Gln Glu Gly Glu Thr Ile Thr Tyr Lys Tyr Val Lys Gly Gly
915 920 925
Ser Trp Asp Gln Glu Gly Leu Ala Asp His Thr Arg Glu Asp Asp Asn
930 935 940
Asp Asp Asp Val Ser Tyr Tyr Gly Tyr Gly Thr Ile Gly Thr Asp Leu
945 950 955 960
Lys Val Thr Val His Asn Glu Gly Asn Asn Thr Met Ile Val Gln Asp
965 970 975
Arg Ile Leu Arg Trp Ile Asp Met Pro Val Val Ile Glu Glu Val Gln
980 985 990
Lys Gln Gly Ser Gln Val Thr Ile Lys Gly Asn Ala Ile Lys Asn Gly
995 1000 1005
Val Leu Thr Ile Asn Gly Glu Arg Val Pro Ile Asp Gly Arg Met Ala
1010 1015 1020
Phe Ser Tyr Thr Phe Ala Pro Ala Ser His Gln Lys Glu Val Leu Ile
1025 1030 1035 1040
His Ile Glu Pro Ser Ala Glu Ser Lys Thr Ala Ile Phe Asn Asn Asp
1045 1050 1055
Gly Gly Ala Ile Ala Lys Asn Thr Lys Asp Tyr Val Leu Asn Leu Glu
1060 1065 1070
Thr Lys Gln Phe Lys Lys Leu Leu Glu Ser Thr Ser Arg Ala Ala Ala
1075 1080 1085
Gly Pro Ser Ile Phe His Pro Gly Gly Val Pro Gly
1090 1095 1100

<210> 91
<211> 1650
<212> DNA

<213> Bacterial

<400> 91
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accatgatgc agtattttga atggtacttg ccggatgatg gcacgttatg gaccaaagtg 180
gccaatgaag ccaacaactt atccagcctt ggcatcaccg ctctttggct gccgcccgct 240
tataaaggaa caagccgcag cgacgtaggg tacggagtat acgacttgta tgacctcggc 300
gaattcaatc aaaaagggac cgtccgcaca aaatacggaa caaaagctca atatcttcaa 360
gccattcaag ccgcccacgc cgctggaatg caagtgtacg ccgatgtcgt gttcgaccat 420
aaaggcggcg ccgacggcac ggaatgggtg gacgccgtcg aagtcaatcc gtccgaccgc 480
aaccaagaaa tctcgggcac ctatcaaatc caagcatgga cgaaatttga ttttcccggg 540
cggggcaaca cctactccag ctttaagtgg cgctggtacc attttgacgg cgttgattgg 600
gacgaaagcc gaaaattgag ccgcatttac aaattccgcg gcatcggcaa agcgtgggat 660
tgggaagtag acacggaaaa cggaaactat gactacttaa tgtatgccga cttggacatg 720
gaccatcctg aagtggttac ggaactgaaa aactggggca aatggtatgt caacacaacg 780
aacattgatg ggttccggct tgatgccgtc aagcatatta agttcagttt ttttcctgat 840
tggttgtcgt atgtgcgttc tcagactggc aagccgctat ttaccgtcgg ggaatattgg 900
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ggtgactatt atggcatccc acaatataac attccttcgc tgaaaagcaa aatcgatccg 1260
ctcctcatcg cgcgcaggga ttatgcttac ggaacgcaac atgattatct tgatcactcc 1320
gacatcatcg ggtggacaag ggaaggcgtc actgaaaaac caggatccgg actggccgca 1380
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aaagtgttct atgaccttac cggcaaccgg agtgacaccg tcaccatcaa cagtgatgga 1500
tggggagaat tcaaagtcaa tggcggttcg gtttcggttt gggttcctag aaaaacgacc 1560
gtctctacca tcgcttggcc gatcacaacc cgaccgtgga ctggtgaatt cgtccgttgg 1620
accgaaccac ggttggtggc atggccttga 1650

<210> 92
<211> 549
<212> PRT
<213> Bacterial

<400> 92
Val Leu Thr Phe His Arg Ile Ile Arg Lys Gly Trp Met Phe Leu Leu
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20 25 30
Lys Ala Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp
35 40 45
Tyr Leu Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala
50 55 60
Asn Asn Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala
65 70 75 80
Tyr Lys Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu
85 90 95
Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr
100 105 110
Gly Thr Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala
115 120 125
Gly Met Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala
130 135 140
Asp Gly Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg

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145                 150                 155                 160
Asn Gln Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe
                165                 170                 175
Asp Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp
            180                 185                 190
Tyr His Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg
        195                 200                 205
Ile Tyr Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp
    210                 215                 220
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met
225                 230                 235                 240
Asp His Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr
                245                 250                 255
Val Asn Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His
            260                 265                 270
Ile Lys Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln
        275                 280                 285
Thr Gly Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile
    290                 295                 300
Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asn Gly Thr Met Ser Leu
305                 310                 315                 320
Phe Asp Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly
                325                 330                 335
Gly Ala Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp
            340                 345                 350
Gln Pro Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro
        355                 360                 365
Gly Gln Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala
    370                 375                 380
Tyr Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr
385                 390                 395                 400
Gly Asp Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser
                405                 410                 415
Lys Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr
            420                 425                 430
Gln His Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu
        435                 440                 445
Gly Val Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp
    450                 455                 460
Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly
465                 470                 475                 480
Lys Val Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile
                485                 490                 495
Asn Ser Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser
            500                 505                 510
Val Trp Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Trp Pro Ile
        515                 520                 525
Thr Thr Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg
    530                 535                 540
Leu Val Ala Trp Pro
545
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<210> 93
<211> 1545
<212> DNA
<213> Bacterial

<400> 93
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ttattgttcg ttcagctgtt ttcatttagt gcaaccgcta gcgccaatgg aacggtgaac 180
agtagtcctg tggttaatgg aaacgaagtc acgtttctat atggaggaac aggaaacgag 240
cagtctgtgt tactggcagg ctcctttaat gattggcaga aagatggtga caagaagatt 300
gcactaacaa aaggcgacaa taacgtctgg tctgtcacgc aaacacttca agatgggaca 360
tatacgtata agtttgttgt agatggtcaa tgggtggcgg atccgcttaa cccgaatcaa 420
gtagacgacg gttacggcgg ccgtaatagt gtcgttgttg tcgggacacc ggtgcaacaa 480
gaacggacag tgacgcttgt tggtaactta caagacgaat taggtcatac gagcgaatgg 540
gatccgaaag cgacagctac agtgatgaaa aaggaaggga acgggttata tacgtttaca 600
ggtacacttc cagccggaac gtacgagtat aaaattgcga ttaatggcag ctgggacgaa 660
aactatggtg tcggcggccg cgatggcggg aatattaagc tgctattaaa tgaacaaaca 720
acggttacat tttattacaa cgacagaacg catgcgattg cggattcgac ttggtatgca 780
ccaattctaa aagaaaagca gccgcggctc gttggaacga ttttaccagc tattggttat 840
gaaacagacg tgaacggttg gacgccgcaa acatcaacgg cgttgttgtc agatgatgat 900
tttgattcca tttatacgtt taaggcgcgt gtgccaaaag ggacatatga atataaagta 960
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tacaatccaa gcggttcgga tggtatcgtc caaaaagacc gtttgaagca taatacgtgg 1140
gattcgttgt atcgccaacc gtttggtgcg gtgaaagctg ggacagaagt gacccttcgt 1200
ttatcagcga aaaaaggtga tttgacaaaa gcggatgtat atgtaaaaaa tacgacaacc 1260
ggcacagcga aactatattc gatgaaaaaa gccggtgttc ttggcgaaga agaatattgg 1320
gaagcgacat tcacaccgga tgtgaaagga gtatacggtt ataaatttat tgcggtagat 1380
gctggaacga aagcagaata cggggaagat acacaagaag ggcagtgggg aaaagcagta 1440
gataaaaatg cagagctgtt ccaattaacg gtgtacgacc catcctacca aacaccggat 1500
tggatgaaag aagcagttgt atatcaaatt ttccctgatc caaag 1545

<210> 94
<211> 515
<212> PRT
<213> Bacterial

<400> 94
Met Lys Ser Phe Ala Phe Met Pro Ile Leu Phe Tyr Ala Asn Asp Phe
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20 25 30
Arg Phe Thr Tyr Phe Ser Ile Phe Leu Leu Phe Val Gln Leu Phe Ser
35 40 45
Phe Ser Ala Thr Ala Ser Ala Asn Gly Thr Val Asn Ser Ser Pro Val
50 55 60
Val Asn Gly Asn Glu Val Thr Phe Leu Tyr Gly Gly Thr Gly Asn Glu
65 70 75 80
Gln Ser Val Leu Leu Ala Gly Ser Phe Asn Asp Trp Gln Lys Asp Gly
85 90 95
Asp Lys Lys Ile Ala Leu Thr Lys Gly Asp Asn Asn Val Trp Ser Val
100 105 110
Thr Gln Thr Leu Gln Asp Gly Thr Tyr Thr Tyr Lys Phe Val Val Asp
115 120 125
Gly Gln Trp Val Ala Asp Pro Leu Asn Pro Asn Gln Val Asp Asp Gly
130 135 140
Tyr Gly Gly Arg Asn Ser Val Val Val Val Gly Thr Pro Val Gln Gln
145 150 155 160
Glu Arg Thr Val Thr Leu Val Gly Asn Leu Gln Asp Glu Leu Gly His
165 170 175
Thr Ser Glu Trp Asp Pro Lys Ala Thr Ala Thr Val Met Lys Lys Glu

```
            180                 185                 190
Gly Asn Gly Leu Tyr Thr Phe Thr Gly Thr Leu Pro Ala Gly Thr Tyr
        195                 200                 205
Glu Tyr Lys Ile Ala Ile Asn Gly Ser Trp Asp Glu Asn Tyr Gly Val
    210                 215                 220
Gly Gly Arg Asp Gly Gly Asn Ile Lys Leu Leu Leu Asn Glu Gln Thr
225                 230                 235                 240
Thr Val Thr Phe Tyr Tyr Asn Asp Arg Thr His Ala Ile Ala Asp Ser
                245                 250                 255
Thr Trp Tyr Ala Pro Ile Leu Lys Glu Lys Gln Pro Arg Leu Val Gly
            260                 265                 270
Thr Ile Leu Pro Ala Ile Gly Tyr Glu Thr Asp Val Asn Gly Trp Thr
        275                 280                 285
Pro Gln Thr Ser Thr Ala Leu Leu Ser Asp Asp Asp Phe Asp Ser Ile
    290                 295                 300
Tyr Thr Phe Lys Ala Arg Val Pro Lys Gly Thr Tyr Glu Tyr Lys Val
305                 310                 315                 320
Val Leu Gly Asn Asp Trp Thr Tyr Glu Asn Tyr Pro Gln Asp Asn Ala
                325                 330                 335
Lys Leu Asn Val Leu Glu Glu Thr Thr Ile Thr Phe Phe Phe Asn Ala
            340                 345                 350
Lys Thr Lys Val Val Tyr Thr Asp Tyr Asn Pro Ser Gly Ser Asp Gly
        355                 360                 365
Ile Val Gln Lys Asp Arg Leu Lys His Asn Thr Trp Asp Ser Leu Tyr
    370                 375                 380
Arg Gln Pro Phe Gly Ala Val Lys Ala Gly Thr Glu Val Thr Leu Arg
385                 390                 395                 400
Leu Ser Ala Lys Lys Gly Asp Leu Thr Lys Ala Asp Val Tyr Val Lys
                405                 410                 415
Asn Thr Thr Thr Gly Thr Ala Lys Leu Tyr Ser Met Lys Lys Ala Gly
            420                 425                 430
Val Leu Gly Glu Glu Glu Tyr Trp Glu Ala Thr Phe Thr Pro Asp Val
        435                 440                 445
Lys Gly Val Tyr Gly Tyr Lys Phe Ile Ala Val Asp Ala Gly Thr Lys
    450                 455                 460
Ala Glu Tyr Gly Glu Asp Thr Gln Glu Gly Gln Trp Gly Lys Ala Val
465                 470                 475                 480
Asp Lys Asn Ala Glu Leu Phe Gln Leu Thr Val Tyr Asp Pro Ser Tyr
                485                 490                 495
Gln Thr Pro Asp Trp Met Lys Glu Ala Val Val Tyr Gln Ile Phe Pro
            500                 505                 510
Asp Pro Lys
        515
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<210> 95
<211> 1524
<212> DNA
<213> Bacterial

<400> 95

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atgtatacac tattcatccg ttcatatttt gatactgatg gtgatggtgt aggagacttt      60
agtggagttg ctgaaaaggt agattatcta aaatctcttg gagtagatac agtctggttt     120
ttaccattta ataaaagtaa atcttatcat ggatatgatg ttgaagatta ctatgatgta     180
gaaccagatt atggaacact acaagatctt gataatatga taaaagttct aaatgaaaat     240
ggaataaagg tagtaatgga tcttgttgtt aatcatacgt cggatacaca tccatggttt     300
cttgatgcag ttgaaaatac tactaattct ccatattgga actattacat tatgagcttg     360
gatgagcctc aaaataagaa tcattggcat tataaggtta attcaaaagg acaaactgtg     420
```

```
tggtattttg gattgtttga ttcatcaatg ccggacctta attacgacaa ccctaaagta     480
atggatgaag tgaaaaaaat aatagatttt tgggcagata tgggagtaga tggatttaga     540
ttagatgcag caaaacatta ttatggattt gactggagcg atggaattga acagtcagca     600
agcgttgcaa aagagataga agactatata aaagataaac taggggaaaa tgcaatagtt     660
gtgagtgagg tttacgatgg agattcaaat gttcttttaa aatttgctcc aatgcctgtg     720
tttaatttta gttttatgta caatttgaga ggaaattttg aagggagaga taacttaatt     780
tcagactcta ttagttgggt tgattcctcg ttgtataatt taaatgtttt tcattttcca     840
tttattgata gtcatgatct tgacagattt atttctgagc ttgtagatag taaatatcag     900
ggagatgtaa tatctgccac aaaacaatat ttgctagtta atgctttact actctcatta     960
acaggcatgc caactattta ctatggtgat gaaataggac ttaggggatg gaagtggcat    1020
tcagaaccat gggatatacc tgtgcgtgag ccaatgcaat ggtataagga tcaaaaaggg    1080
aacggtcaaa cttattggac aaaagagttt tacgaaggta ttactgaagg aagtgctaat    1140
gaagatggag caatatacga tgatccagat gatggagtat ctgtagaaga acaagaaaat    1200
ggatattcta ttttaaactt ttttaaagaa tttatcaact tacgaaaaga ttatccggca    1260
cttgcttttg gaagtactac gattgagaga gattggaaaa acttgtatgt tttgaaaaag    1320
tcgtataact tccaggatgt tcttgtatta attaaccttg atccaacgta ttcaaataca    1380
tacgaagttc cagaagggta taaatgggtg tggtatgcat tttttgatgg tgacaactat    1440
gaatttggag caaaagatga aatgatttta cagaatacaa gttggacgat aaatccaagg    1500
caaatttata tatttgtaaa gtaa                                          1524
```

<210> 96
<211> 507
<212> PRT
<213> Bacterial

<400> 96

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Met Tyr Thr Leu Phe Ile Arg Ser Tyr Phe Asp Thr Asp Gly Asp Gly
 1               5                  10                  15
Val Gly Asp Phe Ser Gly Val Ala Glu Lys Val Asp Tyr Leu Lys Ser
            20                  25                  30
Leu Gly Val Asp Thr Val Trp Phe Leu Pro Phe Asn Lys Ser Lys Ser
        35                  40                  45
Tyr His Gly Tyr Asp Val Glu Asp Tyr Tyr Asp Val Glu Pro Asp Tyr
    50                  55                  60
Gly Thr Leu Gln Asp Leu Asp Asn Met Ile Lys Val Leu Asn Glu Asn
65                  70                  75                  80
Gly Ile Lys Val Val Met Asp Leu Val Val Asn His Thr Ser Asp Thr
                85                  90                  95
His Pro Trp Phe Leu Asp Ala Val Glu Asn Thr Thr Asn Ser Pro Tyr
            100                 105                 110
Trp Asn Tyr Tyr Ile Met Ser Leu Asp Glu Pro Gln Asn Lys Asn His
        115                 120                 125
Trp His Tyr Lys Val Asn Ser Lys Gly Gln Thr Val Trp Tyr Phe Gly
    130                 135                 140
Leu Phe Asp Ser Ser Met Pro Asp Leu Asn Tyr Asp Asn Pro Lys Val
145                 150                 155                 160
Met Asp Glu Val Lys Lys Ile Ile Asp Phe Trp Ala Asp Met Gly Val
                165                 170                 175
Asp Gly Phe Arg Leu Asp Ala Ala Lys His Tyr Tyr Gly Phe Asp Trp
            180                 185                 190
Ser Asp Gly Ile Glu Gln Ser Ala Ser Val Ala Lys Glu Ile Glu Asp
        195                 200                 205
Tyr Ile Lys Asp Lys Leu Gly Glu Asn Ala Ile Val Val Ser Glu Val
    210                 215                 220
Tyr Asp Gly Asp Ser Asn Val Leu Leu Lys Phe Ala Pro Met Pro Val
225                 230                 235                 240
Phe Asn Phe Ser Phe Met Tyr Asn Leu Arg Gly Asn Phe Glu Gly Arg
```

```
                245                 250                 255
Asp Asn Leu Ile Ser Asp Ser Ile Ser Trp Val Asp Ser Ser Leu Tyr
            260                 265                 270
Asn Leu Asn Val Phe His Phe Pro Phe Ile Asp Ser His Asp Leu Asp
        275                 280                 285
Arg Phe Ile Ser Glu Leu Val Asp Ser Lys Tyr Gln Gly Asp Val Ile
    290                 295                 300
Ser Ala Thr Lys Gln Tyr Leu Leu Val Asn Ala Leu Leu Leu Ser Leu
305                 310                 315                 320
Thr Gly Met Pro Thr Ile Tyr Tyr Gly Asp Glu Ile Gly Leu Arg Gly
                325                 330                 335
Trp Lys Trp His Ser Glu Pro Trp Asp Ile Pro Val Arg Glu Pro Met
            340                 345                 350
Gln Trp Tyr Lys Asp Gln Lys Gly Asn Gly Gln Thr Tyr Trp Thr Lys
        355                 360                 365
Glu Phe Tyr Glu Gly Ile Thr Glu Gly Ser Ala Asn Glu Asp Gly Ala
    370                 375                 380
Ile Tyr Asp Asp Pro Asp Asp Gly Val Ser Val Glu Glu Gln Glu Asn
385                 390                 395                 400
Gly Tyr Ser Ile Leu Asn Phe Phe Lys Glu Phe Ile Asn Leu Arg Lys
                405                 410                 415
Asp Tyr Pro Ala Leu Ala Phe Gly Ser Thr Thr Ile Glu Arg Asp Trp
            420                 425                 430
Lys Asn Leu Tyr Val Leu Lys Lys Ser Tyr Asn Phe Gln Asp Val Leu
        435                 440                 445
Val Leu Ile Asn Leu Asp Pro Thr Tyr Ser Asn Thr Tyr Glu Val Pro
    450                 455                 460
Glu Gly Tyr Lys Trp Val Trp Tyr Ala Phe Phe Asp Gly Asp Asn Tyr
465                 470                 475                 480
Glu Phe Gly Ala Lys Asp Glu Met Ile Leu Gln Asn Thr Ser Trp Thr
                485                 490                 495
Ile Asn Pro Arg Gln Ile Tyr Ile Phe Val Lys
            500                 505
```

<210> 97
<211> 2931
<212> DNA
<213> Bacterial

<400> 97

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atgaggaaga agatgtcgca ttcaagattt acttttcttt tgatcttagc acttttttatt      60
ttcttctccg gttgtatttc agaagttaaa agcgaaagcc agctactaaa ttcaaagcaa      120
aaggtccttg taaaagtaaa tgttaatacg ccatttattg agaatgctac tactaatacg      180
tggagtgttt caaaagaatc ttttattgat tatcttagta aagtgattat tactgttaag      240
gatgtaaatg atcagattgt atttactaag gaaacaacga acaaaacaaa tatttatttt      300
gaaattgaac ttcttcctgg aacttataca tttgaggtaa aaggatatga ggaagattta      360
gttatatttt caggggaaaa agttaatcag atcatagatg agaaaaataa tattgttaat      420
gtcgaaactt tttttgttaa tggaatagtt aggacaataa ttgaagttga cgatattatt      480
tataaaaatt atgatattac atcggcaacg ttgatcttca aaaaagatac agcacaagaa      540
gattatgaag aggtacctgt aacacttaca ggtacttcca ctttaattaa taaagaatta      600
tatcctggta tgtggactgt aaaatttgaa gttgatctta aatcaaagga tgcaagtatg      660
ttaccagaaa aagttcatct tgaaaatgaa tttagcatag aagtgcttcc agcaaagaca      720
aaaagtttaa catttaatgt agtctttgat acagaggtta atgaaccgaa attagtagtt      780
gtatttccgc aaattgagtt gccttttgtg gatcctgtaa caaatttaag tggagagata      840
aatgaattag aagggaatct ttcaatgaat tgggactatt cagatccaaa tgcagaattt      900
tatgtgtata aagaattaga ggaacaagga gaatatttgt atgaatttgt tggaaaaaca      960
cgcgagaaaa gttatacaat agaaaatttt accaagcaag aattcgataa atttagtgga     1020
```

```
atcgctatta atgtttatgc caacggtaaa gagagtggat tagttgttct aaaaaaagaa    1080
aatattaaac ttatagattt agaaagtgtt gacagtataa gtgctactta taacgttgat    1140
acgaatgagc ttaagttgga ttggaattat accaattcaa gtgttacttt tgaagttttg    1200
aaaaaaggta taaatagcaa tgaatacgaa ataatttctc aactaacaca aaattctttt    1260
tcaacagaat tcacaggcag gcaatttttgg gatcttgaga aaattgcgat tagagtagtt    1320
gctaatggat ttgaaagtaa gattaatgag atttcaagag atgatataac tataacatca    1380
ttgaatcttc ctcttacatc gtctactatg tatacactat tcatccgttc atattttgat    1440
actgatggtg atggtgtagg agactttagt ggagttgctg aaaaggtaga ttatctaaaa    1500
tctcttggag tagatacagt ctggttttta ccatttaata aaagtaaatc ttatcatgga    1560
tatgatgttg aagattacta tgatgtagaa ccagattatg gaacactaca agatcttgat    1620
aatatgataa aagttctaaa tgaaaatgga ataaaggtag taatggatct tgttgttaat    1680
catacgtcgg atacacatcc atggtttctt gatgcagttg aaaatactac taattctcca    1740
tattggaact attacattat gagcttggat gagcctcaaa ataagaatca ttggcattat    1800
aaggttaatt caaaaggaca aactgtgtgg tattttggat tgtttgattc atcaatgccg    1860
gaccttaatt acgacaaccc taaagtaatg gatgaagtga aaaaaataat agatttttgg    1920
gcagatatgg gagtagatgg atttagatta gatgcagcaa aacattatta tggatttgac    1980
tggagcgatg gaattgaaca gtcagcaagc gttgcaaaag agatagaaga ctatataaaa    2040
gataaactag gggaaaatgc aatagttgtg agtgaggttt acgatggaga ttcaaatgtt    2100
cttttaaaat ttgctccaat gcctgtgttt aattttagtt ttatgtacaa tttgagagga    2160
aattttgaag ggagagataa cttaatttca gactctatta gttgggttga ttcctcgttg    2220
tataatttaa atgtttttca ttttccattt attgatagtc atgatcttga cagatttatt    2280
tctgagcttg tagatagtaa atatcaggga gatgtaatat ctgccacaaa acaatatttg    2340
ctagttaatg ctttactact ctcattaaca ggcatgccaa ctatttacta tggtgatgaa    2400
ataggactta ggggatggaa gtggcattca gaaccatggg atatacctgt gcgtgagcca    2460
atgcaatggt ataaggatca aaaagggaac ggtcaaactt attggacaaa agagttttac    2520
gaaggtatta ctgaaggaag tgctaatgaa gatggagcaa tatacgatga tccagatgat    2580
ggagtatctg tagaagaaca agaaaatgga tattctattt taaacttttt taaagaattt    2640
atcaacttac gaaaagatta tccggcactt gcttttggaa gtactacgat tgagagagat    2700
tggaaaaact tgtatgtttt gaaaaagtcg tataacttcc aggatgttct tgtattaatt    2760
aaccttgatc caacgtattc aaatacatac gaagttccag aagggtataa atgggtgtgg    2820
tatgcatttt ttgatggtga caactatgaa tttggagcaa aagatgaaat gattttacag    2880
aatacaagtt ggacgataaa tccaaggcaa atttatatat ttgtaaagta a              2931
```

<210> 98
<211> 976
<212> PRT
<213> Bacterial

<400> 98

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Met Arg Lys Lys Met Ser His Ser Arg Phe Thr Phe Leu Leu Ile Leu
 1               5                  10                  15
Ala Leu Phe Ile Phe Phe Ser Gly Cys Ile Ser Glu Val Lys Ser Glu
            20                  25                  30
Ser Gln Leu Leu Asn Ser Lys Gln Lys Val Leu Val Lys Val Asn Val
        35                  40                  45
Asn Thr Pro Phe Ile Glu Asn Ala Thr Thr Asn Thr Trp Ser Val Ser
    50                  55                  60
Lys Glu Ser Phe Ile Asp Tyr Leu Ser Lys Val Ile Ile Thr Val Lys
65                  70                  75                  80
Asp Val Asn Asp Gln Ile Val Phe Thr Lys Glu Thr Thr Asn Lys Thr
                85                  90                  95
Asn Ile Tyr Phe Glu Ile Glu Leu Leu Pro Gly Thr Tyr Thr Phe Glu
            100                 105                 110
Val Lys Gly Tyr Glu Glu Asp Leu Val Ile Phe Ser Gly Glu Lys Val
        115                 120                 125
Asn Gln Ile Ile Asp Glu Lys Asn Asn Ile Val Asn Val Glu Thr Phe
    130                 135                 140
```

```
Phe Val Asn Gly Ile Val Arg Thr Ile Ile Glu Val Asp Asp Ile Ile
145                 150                 155                 160
Tyr Lys Asn Tyr Asp Ile Thr Ser Ala Thr Leu Ile Phe Lys Lys Asp
                165                 170                 175
Thr Ala Gln Glu Asp Tyr Glu Glu Val Pro Val Thr Leu Thr Gly Thr
            180                 185                 190
Ser Thr Leu Ile Asn Lys Glu Leu Tyr Pro Gly Met Trp Thr Val Lys
        195                 200                 205
Phe Glu Val Asp Leu Lys Ser Lys Asp Ala Ser Met Leu Pro Glu Lys
    210                 215                 220
Val His Leu Glu Asn Glu Phe Ser Ile Glu Val Leu Pro Ala Lys Thr
225                 230                 235                 240
Lys Ser Leu Thr Phe Asn Val Val Phe Asp Thr Glu Val Asn Glu Pro
                245                 250                 255
Lys Leu Val Val Val Phe Pro Gln Ile Glu Leu Pro Phe Val Asp Pro
            260                 265                 270
Val Thr Asn Leu Ser Gly Glu Ile Asn Glu Leu Glu Gly Asn Leu Ser
        275                 280                 285
Met Asn Trp Asp Tyr Ser Asp Pro Asn Ala Glu Phe Tyr Val Tyr Lys
    290                 295                 300
Glu Leu Glu Glu Gln Gly Glu Tyr Leu Tyr Glu Phe Val Gly Lys Thr
305                 310                 315                 320
Arg Glu Lys Ser Tyr Thr Ile Glu Asn Phe Thr Lys Gln Glu Phe Asp
                325                 330                 335
Lys Phe Ser Gly Ile Ala Ile Asn Val Tyr Ala Asn Gly Lys Glu Ser
            340                 345                 350
Gly Leu Val Val Leu Lys Lys Glu Asn Ile Lys Leu Ile Asp Leu Glu
        355                 360                 365
Ser Val Asp Ser Ile Ser Ala Thr Tyr Asn Val Asp Thr Asn Glu Leu
    370                 375                 380
Lys Leu Asp Trp Asn Tyr Thr Asn Ser Ser Val Thr Phe Glu Val Leu
385                 390                 395                 400
Lys Lys Gly Ile Asn Ser Asn Glu Tyr Glu Ile Ile Ser Gln Leu Thr
                405                 410                 415
Gln Asn Ser Phe Ser Thr Glu Phe Thr Gly Arg Gln Phe Trp Asp Leu
            420                 425                 430
Glu Lys Ile Ala Ile Arg Val Val Ala Asn Gly Phe Glu Ser Lys Ile
        435                 440                 445
Asn Glu Ile Ser Arg Asp Asp Ile Thr Ile Thr Ser Leu Asn Leu Pro
    450                 455                 460
Leu Thr Ser Ser Thr Met Tyr Thr Leu Phe Ile Arg Ser Tyr Phe Asp
465                 470                 475                 480
Thr Asp Gly Asp Gly Val Gly Asp Phe Ser Gly Val Ala Glu Lys Val
                485                 490                 495
Asp Tyr Leu Lys Ser Leu Gly Val Asp Thr Val Trp Phe Leu Pro Phe
            500                 505                 510
Asn Lys Ser Lys Ser Tyr His Gly Tyr Asp Val Glu Asp Tyr Tyr Asp
        515                 520                 525
Val Glu Pro Asp Tyr Gly Thr Leu Gln Asp Leu Asp Asn Met Ile Lys
    530                 535                 540
Val Leu Asn Glu Asn Gly Ile Lys Val Val Met Asp Leu Val Val Asn
545                 550                 555                 560
His Thr Ser Asp Thr His Pro Trp Phe Leu Asp Ala Val Glu Asn Thr
                565                 570                 575
Thr Asn Ser Pro Tyr Trp Asn Tyr Tyr Ile Met Ser Leu Asp Glu Pro
            580                 585                 590
Gln Asn Lys Asn His Trp His Tyr Lys Val Asn Ser Lys Gly Gln Thr
```

595 600 605
Val Trp Tyr Phe Gly Leu Phe Asp Ser Ser Met Pro Asp Leu Asn Tyr
610 615 620
Asp Asn Pro Lys Val Met Asp Glu Val Lys Lys Ile Ile Asp Phe Trp
625 630 635 640
Ala Asp Met Gly Val Asp Gly Phe Arg Leu Asp Ala Ala Lys His Tyr
645 650 655
Tyr Gly Phe Asp Trp Ser Asp Gly Ile Glu Gln Ser Ala Ser Val Ala
660 665 670
Lys Glu Ile Glu Asp Tyr Ile Lys Asp Lys Leu Gly Glu Asn Ala Ile
675 680 685
Val Val Ser Glu Val Tyr Asp Gly Asp Ser Asn Val Leu Leu Lys Phe
690 695 700
Ala Pro Met Pro Val Phe Asn Phe Ser Phe Met Tyr Asn Leu Arg Gly
705 710 715 720
Asn Phe Glu Gly Arg Asp Asn Leu Ile Ser Asp Ser Ile Ser Trp Val
725 730 735
Asp Ser Ser Leu Tyr Asn Leu Asn Val Phe His Phe Pro Phe Ile Asp
740 745 750
Ser His Asp Leu Asp Arg Phe Ile Ser Glu Leu Val Asp Ser Lys Tyr
755 760 765
Gln Gly Asp Val Ile Ser Ala Thr Lys Gln Tyr Leu Leu Val Asn Ala
770 775 780
Leu Leu Leu Ser Leu Thr Gly Met Pro Thr Ile Tyr Tyr Gly Asp Glu
785 790 795 800
Ile Gly Leu Arg Gly Trp Lys Trp His Ser Glu Pro Trp Asp Ile Pro
805 810 815
Val Arg Glu Pro Met Gln Trp Tyr Lys Asp Gln Lys Gly Asn Gly Gln
820 825 830
Thr Tyr Trp Thr Lys Glu Phe Tyr Glu Gly Ile Thr Glu Gly Ser Ala
835 840 845
Asn Glu Asp Gly Ala Ile Tyr Asp Asp Pro Asp Asp Gly Val Ser Val
850 855 860
Glu Glu Gln Glu Asn Gly Tyr Ser Ile Leu Asn Phe Phe Lys Glu Phe
865 870 875 880
Ile Asn Leu Arg Lys Asp Tyr Pro Ala Leu Ala Phe Gly Ser Thr Thr
885 890 895
Ile Glu Arg Asp Trp Lys Asn Leu Tyr Val Leu Lys Lys Ser Tyr Asn
900 905 910
Phe Gln Asp Val Leu Val Leu Ile Asn Leu Asp Pro Thr Tyr Ser Asn
915 920 925
Thr Tyr Glu Val Pro Glu Gly Tyr Lys Trp Val Trp Tyr Ala Phe Phe
930 935 940
Asp Gly Asp Asn Tyr Glu Phe Gly Ala Lys Asp Glu Met Ile Leu Gln
945 950 955 960
Asn Thr Ser Trp Thr Ile Asn Pro Arg Gln Ile Tyr Ile Phe Val Lys
965 970 975

<210> 99
<211> 1536
<212> DNA
<213> Bacterial

<400> 99
atgtacacac tcttcatccg ctctttttac gatacaaaca acgacggtgt aggtgactac 60
aacggtgttg cccaaaaagt agactatctc aaaacgcttg gagtggatac agtttggttc 120
ttgccgttca acaaagcaaa atcgtaccac ggttacgatg ttgaagacta ctacgatgta 180

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gaacctgact atggaacata cgcacaactt gaaaatatga taaagacact caatcagaac     240
ggaattcgtg ttgttatgga cttggttgtg aaccacactt ccgatacaca ctcgtggttt     300
ctggatgccg ttgagaacac aacgaattcg aaatattgga gctactacat aatgacactt     360
gaaaatagag acggttggaa tcactggcat tggaagataa actcaaaagg gcaaaaagtt     420
tactacttcg gactgtttga ctcatcaatg cccgatttga atttcgacaa tccacaagtg     480
atgaacgaaa tcaagagaat aatcgatttc tggataacag ttggtgtgga tggtttcaga     540
cttgatgcac caaagcacta caaaggctgg gattgggacg acggcatttc aggttcagca     600
gcaatcgcga gggaaataga aagttacatc aggagcaagt taggaaacga tgcgatagtt     660
gtcggggaag tgtacgatgg aaatccatcg gttctttcac aatttgcacc gatgccggcg     720
ttcaacttca cattcatgta tggaataaca ggcaaccatg aggggaaaga taacctgctg     780
ggagaaacaa tttcatgggt taatggagcg agttattatc tcaacgtaaa acatttcccg     840
ttcatagaca atcacgattt gaacagatgg atatcgatac ttatcgacca aaagtatagt     900
ggaaacacac aagttggtac gaagcagtat attttaacaa atgcgctctt gctttcctta     960
aacggtatgc ctgttattta ttatgggaat gaaataggct tgagaggatg gaaatgggga    1020
caagacccgt gggatttgcc ggtgagagag ccgatgcagt ggtacgcaag tcaaagtgga    1080
gctgggcaga catggtggac aaagcctgtc taccagcaaa aaggaatcac atttggaaat    1140
gcaaacgtcg atggtgcgat gtacgatgat ccaaatgatg gggtttcagt agaagagcag    1200
atgaatggtt acacgataaa taacttcttt aaacaattca taaccctgag gaagacatat    1260
ccggctctat cgaaaggttc gataacgata gaacgcgact ggaagaacct gtacgttatc    1320
aaacgagtct acggaaatca ggaagtgctt gtattgataa acttagaccc aacttggccg    1380
aacaattaca cgttaccagg tggatacagg tgggtctggt atgcgttctt taatgggagt    1440
ttgtttgaat ttggcaataa aaacgaatca ccactgagcc aagataccaa ctggacagtc    1500
aatccaaggc aagtgtatgt gtttgtgaag gactaa                               1536

<210> 100
<211> 511
<212> PRT
<213> Bacterial

<400> 100
Met Tyr Thr Leu Phe Ile Arg Ser Phe Tyr Asp Thr Asn Asn Asp Gly
 1               5                  10                  15
Val Gly Asp Tyr Asn Gly Val Ala Gln Lys Val Asp Tyr Leu Lys Thr
            20                  25                  30
Leu Gly Val Asp Thr Val Trp Phe Leu Pro Phe Asn Lys Ala Lys Ser
        35                  40                  45
Tyr His Gly Tyr Asp Val Glu Asp Tyr Tyr Asp Val Glu Pro Asp Tyr
    50                  55                  60
Gly Thr Tyr Ala Gln Leu Glu Asn Met Ile Lys Thr Leu Asn Gln Asn
65                  70                  75                  80
Gly Ile Arg Val Val Met Asp Leu Val Val Asn His Thr Ser Asp Thr
                85                  90                  95
His Ser Trp Phe Leu Asp Ala Val Glu Asn Thr Thr Asn Ser Lys Tyr
            100                 105                 110
Trp Ser Tyr Tyr Ile Met Thr Leu Glu Asn Arg Asp Gly Trp Asn His
        115                 120                 125
Trp His Trp Lys Ile Asn Ser Lys Gly Gln Lys Val Tyr Tyr Phe Gly
    130                 135                 140
Leu Phe Asp Ser Ser Met Pro Asp Leu Asn Phe Asp Asn Pro Gln Val
145                 150                 155                 160
Met Asn Glu Ile Lys Arg Ile Ile Asp Phe Trp Ile Thr Val Gly Val
                165                 170                 175
Asp Gly Phe Arg Leu Asp Ala Pro Lys His Tyr Lys Gly Trp Asp Trp
            180                 185                 190
Asp Asp Gly Ile Ser Gly Ser Ala Ala Ile Ala Arg Glu Ile Glu Ser
        195                 200                 205
Tyr Ile Arg Ser Lys Leu Gly Asn Asp Ala Ile Val Val Gly Glu Val
```

```
    210                 215                 220
Tyr Asp Gly Asn Pro Ser Val Leu Ser Gln Phe Ala Pro Met Pro Ala
225                 230                 235                 240
Phe Asn Phe Thr Phe Met Tyr Gly Ile Thr Gly Asn His Glu Gly Lys
                245                 250                 255
Asp Asn Leu Leu Gly Glu Thr Ile Ser Trp Val Asn Gly Ala Ser Tyr
            260                 265                 270
Tyr Leu Asn Val Lys His Phe Pro Phe Ile Asp Asn His Asp Leu Asn
        275                 280                 285
Arg Trp Ile Ser Ile Leu Ile Asp Gln Lys Tyr Ser Gly Asn Thr Gln
    290                 295                 300
Val Gly Thr Lys Gln Tyr Ile Leu Thr Asn Ala Leu Leu Leu Ser Leu
305                 310                 315                 320
Asn Gly Met Pro Val Ile Tyr Tyr Gly Asn Glu Ile Gly Leu Arg Gly
                325                 330                 335
Trp Lys Trp Gly Gln Asp Pro Trp Asp Leu Pro Val Arg Glu Pro Met
            340                 345                 350
Gln Trp Tyr Ala Ser Gln Ser Gly Ala Gly Gln Thr Trp Trp Thr Lys
        355                 360                 365
Pro Val Tyr Gln Gln Lys Gly Ile Thr Phe Gly Asn Ala Asn Val Asp
    370                 375                 380
Gly Ala Met Tyr Asp Asp Pro Asn Asp Gly Val Ser Val Glu Glu Gln
385                 390                 395                 400
Met Asn Gly Tyr Thr Ile Asn Asn Phe Phe Lys Gln Phe Ile Thr Leu
                405                 410                 415
Arg Lys Thr Tyr Pro Ala Leu Ser Lys Gly Ser Ile Thr Ile Glu Arg
            420                 425                 430
Asp Trp Lys Asn Leu Tyr Val Ile Lys Arg Val Tyr Gly Asn Gln Glu
        435                 440                 445
Val Leu Val Leu Ile Asn Leu Asp Pro Thr Trp Pro Asn Asn Tyr Thr
    450                 455                 460
Leu Pro Gly Gly Tyr Arg Trp Val Trp Tyr Ala Phe Phe Asn Gly Ser
465                 470                 475                 480
Leu Phe Glu Phe Gly Asn Lys Asn Glu Ser Pro Leu Ser Gln Asp Thr
                485                 490                 495
Asn Trp Thr Val Asn Pro Arg Gln Val Tyr Val Phe Val Lys Asp
            500                 505                 510
```

<210> 101
<211> 2136
<212> DNA
<213> Environmental

<400> 101

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ttgcgattct ttccaaagtt aatatcccct tttccgcaaa acaccagaga gtggcagcga      60
agcgcagtat caagagacac tgaacaatta caaaggaaag taataatgat caatttgaaa     120
aaaaacacca ttagcgccct ggtcgcaggt atggtattag gctttgcatc caacgcaatg     180
gcggttccta gaaccgcttt tgtacacctc tttgaatgga aatgggaaga tgttgcacag     240
gagtgtgaaa catttctcgg acctaaaggc tttgccgcag tgcaagtctc tccgccaact     300
aaatctcaca acacggatgc atggtggggc cgttatcaac ccgttagtta tgcttttgaa     360
ggacgcagcg gtaatcgcag ccaatttaaa aatatggtgc aacgttgtaa agctgtaggc     420
gtcgatatat acgtagatgc agtgattaac cacatggcag cctacgacag aaatttccct     480
gatgtaccct atagcagtaa tgactttaac tcctgtacag gagatattga ctataataac     540
cgttggcaaa cacagcattg tgatttagtc ggtcttaatg atctaaaaac aggatctgac     600
tacgtccgcc aaaaaatagc ggattatatg aacgacgcaa tcagtatggg tgtagctggt     660
ttccgtattg atgcagccaa acatatacca gcaggtgata tagctgccat taaaggtaaa     720
ttaaatggta atccatacat cttccaagag gtaattggtg catccggcga acctgttcga     780
```

```
ccgactgaat acacctttat cggtggtgtc acggaatttc aatttgctcg aaaattgggt     840
ccagccttcc gcaatagtaa tattgcttgg ttaaaagaca ttggcagtca aatggaatta     900
tccagtgctg atgccgtaac atttgtaacg aatcatgatg aagagcgtca taacccgaat     960
ggtcctattt ggcacggcgt tcaaggtaat ggttatgcat tagcaaatat tttcacctta    1020
gcttaccctt acggctatcc aaaaatcatg tcaggatact tcttccacgg tgactttaac    1080
gcagctccac caagcagtgg tatacacaca ggaaatgcgt gtggttttga tggcggagac    1140
tgggtatgcg aacacaaatg gcgcggtatt gctaacatgg ttgccttccg caactataca    1200
gcaagcgaat ggcgtatcag taattggtgg caaaacagta acgaccaaat tgcttttggt    1260
cgcggtggtt taggttttgt tgttattaat aaacgtgcta atggtagcat taatcaaagt    1320
tttgatacgg gaatgcctga tggccaatac tgtaacataa tagaagctaa ctttgatgaa    1380
agcaccggcc aatgtagtgc agctacagat tccaacggtc aagccgttat taccgtcagt    1440
ggtgggcaag ctaactttaa tgtagcaggc gatcatgctg ctgcaattca tgttggcgca    1500
aaaattggtg atcaatgtag tggtgatgat tgcccatgta caggatccga ttgtaataat    1560
gatcctaaac ctgattttgc agtaccagca acatcaattt gtacatcaga aaatttacct    1620
acgctatatt actggggagc acagcctaca gatagcttag cgaatgcagc ttggccaggt    1680
gtcgcaatgc aaacaaatgg cgactttaag tgtcatgatt taggtgtcga actaaccaaa    1740
attaacgcca tctttagtga caatggtgca aataaaacag ctgatctaac tgttactggt    1800
gcaggttgtt ataaagacgg gacttggagc accttacaaa attgtggctt tgaaattacc    1860
ggtgcacaaa ccaatccagt cggtggcgac gaagtctggt acttccgagg tactgctaat    1920
gactggggta aagcacaatt agattatgac gcaactagcg gtttgtatta cacaatacaa    1980
agctttaatg gtgaagaagc acctgcgcgt tttaaaattg ataatggtag ttggactgaa    2040
gcttatccaa cagctgatta ccaagttaca gataacaatt cataccgcat taactttaat    2100
agcgatagca aagcgattac agtaaacgca caataa                              2136

<210> 102
<211> 711
<212> PRT
<213> Environmental

<400> 102
Met Arg Phe Phe Pro Lys Leu Ile Ser Pro Phe Pro Gln Asn Thr Arg
 1               5                  10                  15
Glu Trp Gln Arg Ser Ala Val Ser Arg Asp Thr Glu Gln Leu Gln Arg
            20                  25                  30
Lys Val Ile Met Ile Asn Leu Lys Lys Asn Thr Ile Ser Ala Leu Val
        35                  40                  45
Ala Gly Met Val Leu Gly Phe Ala Ser Asn Ala Met Ala Val Pro Arg
    50                  55                  60
Thr Ala Phe Val His Leu Phe Glu Trp Lys Trp Glu Asp Val Ala Gln
65                  70                  75                  80
Glu Cys Glu Thr Phe Leu Gly Pro Lys Gly Phe Ala Ala Val Gln Val
                85                  90                  95
Ser Pro Pro Thr Lys Ser His Asn Thr Asp Ala Trp Trp Gly Arg Tyr
            100                 105                 110
Gln Pro Val Ser Tyr Ala Phe Glu Gly Arg Ser Gly Asn Arg Ser Gln
        115                 120                 125
Phe Lys Asn Met Val Gln Arg Cys Lys Ala Val Gly Val Asp Ile Tyr
    130                 135                 140
Val Asp Ala Val Ile Asn His Met Ala Ala Tyr Asp Arg Asn Phe Pro
145                 150                 155                 160
Asp Val Pro Tyr Ser Ser Asn Asp Phe Asn Ser Cys Thr Gly Asp Ile
                165                 170                 175
Asp Tyr Asn Asn Arg Trp Gln Thr Gln His Cys Asp Leu Val Gly Leu
            180                 185                 190
Asn Asp Leu Lys Thr Gly Ser Asp Tyr Val Arg Gln Lys Ile Ala Asp
        195                 200                 205
Tyr Met Asn Asp Ala Ile Ser Met Gly Val Ala Gly Phe Arg Ile Asp
```

```
    210                 215                 220
Ala Ala Lys His Ile Pro Ala Gly Asp Ile Ala Ala Ile Lys Gly Lys
225                 230                 235                 240
Leu Asn Gly Asn Pro Tyr Ile Phe Gln Glu Val Ile Gly Ala Ser Gly
                245                 250                 255
Glu Pro Val Arg Pro Thr Glu Tyr Thr Phe Ile Gly Gly Val Thr Glu
            260                 265                 270
Phe Gln Phe Ala Arg Lys Leu Gly Pro Ala Phe Arg Asn Ser Asn Ile
        275                 280                 285
Ala Trp Leu Lys Asp Ile Gly Ser Gln Met Glu Leu Ser Ser Ala Asp
    290                 295                 300
Ala Val Thr Phe Val Thr Asn His Asp Glu Glu Arg His Asn Pro Asn
305                 310                 315                 320
Gly Pro Ile Trp His Gly Val Gln Gly Asn Gly Tyr Ala Leu Ala Asn
                325                 330                 335
Ile Phe Thr Leu Ala Tyr Pro Tyr Gly Tyr Pro Lys Ile Met Ser Gly
            340                 345                 350
Tyr Phe Phe His Gly Asp Phe Asn Ala Ala Pro Pro Ser Ser Gly Ile
        355                 360                 365
His Thr Gly Asn Ala Cys Gly Phe Asp Gly Gly Asp Trp Val Cys Glu
    370                 375                 380
His Lys Trp Arg Gly Ile Ala Asn Met Val Ala Phe Arg Asn Tyr Thr
385                 390                 395                 400
Ala Ser Glu Trp Arg Ile Ser Asn Trp Trp Gln Asn Ser Asn Asp Gln
                405                 410                 415
Ile Ala Phe Gly Arg Gly Gly Leu Gly Phe Val Val Ile Asn Lys Arg
            420                 425                 430
Ala Asn Gly Ser Ile Asn Gln Ser Phe Asp Thr Gly Met Pro Asp Gly
        435                 440                 445
Gln Tyr Cys Asn Ile Ile Glu Ala Asn Phe Asp Glu Ser Thr Gly Gln
    450                 455                 460
Cys Ser Ala Ala Thr Asp Ser Asn Gly Gln Ala Val Ile Thr Val Ser
465                 470                 475                 480
Gly Gly Gln Ala Asn Phe Asn Val Ala Gly Asp His Ala Ala Ala Ile
                485                 490                 495
His Val Gly Ala Lys Ile Gly Asp Gln Cys Ser Gly Asp Asp Cys Pro
            500                 505                 510
Cys Thr Gly Ser Asp Cys Asn Asn Asp Pro Lys Pro Asp Phe Ala Val
        515                 520                 525
Pro Ala Thr Ser Ile Cys Thr Ser Glu Asn Leu Pro Thr Leu Tyr Tyr
    530                 535                 540
Trp Gly Ala Gln Pro Thr Asp Ser Leu Ala Asn Ala Ala Trp Pro Gly
545                 550                 555                 560
Val Ala Met Gln Thr Asn Gly Asp Phe Lys Cys His Asp Leu Gly Val
                565                 570                 575
Glu Leu Thr Lys Ile Asn Ala Ile Phe Ser Asp Asn Gly Ala Asn Lys
            580                 585                 590
Thr Ala Asp Leu Thr Val Thr Gly Ala Gly Cys Tyr Lys Asp Gly Thr
        595                 600                 605
Trp Ser Thr Leu Gln Asn Cys Gly Phe Glu Ile Thr Gly Ala Gln Thr
    610                 615                 620
Asn Pro Val Gly Gly Asp Glu Val Trp Tyr Phe Arg Gly Thr Ala Asn
625                 630                 635                 640
Asp Trp Gly Lys Ala Gln Leu Asp Tyr Asp Ala Thr Ser Gly Leu Tyr
                645                 650                 655
Tyr Thr Ile Gln Ser Phe Asn Gly Glu Glu Ala Pro Ala Arg Phe Lys
            660                 665                 670
```

```
Ile Asp Asn Gly Ser Trp Thr Glu Ala Tyr Pro Thr Ala Asp Tyr Gln
        675                 680                 685
Val Thr Asp Asn Asn Ser Tyr Arg Ile Asn Phe Asn Ser Asp Ser Lys
    690                 695                 700
Ala Ile Thr Val Asn Ala Gln
705                 710
```

<210> 103
<211> 1650
<212> DNA
<213> Environmental

<400> 103

```
gtgctaacgt ttcaccgcat cattcgaaaa ggatggatgt tcctgctcgc gtttttgctc      60
actgcctcgc tgttctgccc aacaggacag cccgccaagg ctgccgcacc gtttaacggc     120
accatgatgc agtattttga atggtacttg ccggatgatg gcacgttatg gaccaaagtg     180
gccaatgaag ccaacaactt atccagcctt ggcatcaccg ctctttggct gccgcccgct     240
tacaaaggaa caagccgcag cgacgtaggg tacggagtat acgacttgta tgacctcggc     300
gaattcaatc aaaaagggac cgtccgcaca aaatacggaa caaaagctca atatcttcaa     360
gccattcaag ccgcccacgc cgctggaatg caagtgtacg ccgatgtcgt gttcgaccat     420
aaaggcggcg ccgacggcac ggaatgggtg gacgccgtcg aagtcaatcc gtccgaccgc     480
aaccaagaaa tctcgggcac ctatcaaatc caagcatgga cgaaatttga ttttcccggg     540
cggggcaaca cctactccag ctttaagtgg cgctggtacc attttgacgg cgttgattgg     600
gacgaaagcc gaaaattgag ccgcatttac aaattccgcg gcatcggcaa agcgtgggat     660
tgggaagtag acacggaaaa cggaaactat gactacttaa tgtatgccga ccttgatatg     720
gatcatcccg aagtcgtgac cgagctgaaa aactgggggg aatggtatgt caacacaacg     780
aacattgatg ggttccggct tgatgccgtc aagcatatta agttcagttt ttttcctgat     840
tggttgtcgt atgtgcgttc tcagactggc aagccgctat ttaccgtcgg ggaatattgg     900
agctatgaca tcaacaagtt gcacaattac attacgaaaa caaacggaac gatgtctttg     960
tttgatgccc cgttacacaa caaattttat accgcttcca aatcaggggg cgcatttgat    1020
atgcgcacgt taatgaccaa tactctcatg aaagatcaac cgacattggc cgtcaccttc    1080
gttgataatc atgacaccga acccggccaa gcgctgcagt catgggtcga cccatggttc    1140
aaaccgttgg cttacgcctt tattctaact cggcaggaag gatacccgtg cgtcttttat    1200
ggtgactatt atggcattcc acaatataac attccttcgc tgaaaagcaa aatcgatccg    1260
ctcctcatcg cgcgcaggga ttatgcttac ggaacgcaac atgattatct tgatcactcc    1320
gacatcatcg ggtggacaag ggaaggggtc actgaaaaac caggatccgg gctggccgca    1380
ctgatcaccg atgggccggg aggaagcaaa tggatgtacg ttggcaaaca acacgctgga    1440
aaagtgttct atgaccttac cggcaaccgg agtgacaccg tcaccatcaa cagtgatgga    1500
tgggggggaat tcaaagtcaa tggcggttcg gtttcggttt gggttcctag aaaaacgacc    1560
gtttctacca tcgctcggcc gatcacaacc cgaccgtgga ctggtgaatt cgtccgttgg    1620
accgaaccac ggttggtggc atggccttga                                     1650
```

<210> 104
<211> 549
<212> PRT
<213> Environmental

<400> 104

```
Val Leu Thr Phe His Arg Ile Ile Arg Lys Gly Trp Met Phe Leu Leu
 1               5                  10                  15
Ala Phe Leu Leu Thr Ala Ser Leu Phe Cys Pro Thr Gly Gln Pro Ala
            20                  25                  30
Lys Ala Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp
        35                  40                  45
Tyr Leu Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala
    50                  55                  60
Asn Asn Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala
```

```
65                  70                  75                  80
Tyr Lys Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu
                85                  90                  95
Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr
            100                 105                 110
Gly Thr Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala
        115                 120                 125
Gly Met Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala
    130                 135                 140
Asp Gly Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg
145                 150                 155                 160
Asn Gln Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe
                165                 170                 175
Asp Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp
            180                 185                 190
Tyr His Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg
        195                 200                 205
Ile Tyr Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp
    210                 215                 220
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met
225                 230                 235                 240
Asp His Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Glu Trp Tyr
                245                 250                 255
Val Asn Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His
            260                 265                 270
Ile Lys Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln
        275                 280                 285
Thr Gly Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile
    290                 295                 300
Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asn Gly Thr Met Ser Leu
305                 310                 315                 320
Phe Asp Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly
                325                 330                 335
Gly Ala Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp
            340                 345                 350
Gln Pro Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro
        355                 360                 365
Gly Gln Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala
    370                 375                 380
Tyr Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr
385                 390                 395                 400
Gly Asp Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser
                405                 410                 415
Lys Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr
            420                 425                 430
Gln His Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu
        435                 440                 445
Gly Val Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp
    450                 455                 460
Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly
465                 470                 475                 480
Lys Val Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile
                485                 490                 495
Asn Ser Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser
            500                 505                 510
Val Trp Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile
        515                 520                 525
```

```
Thr Thr Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg
    530                 535                 540
Leu Val Ala Trp Pro
545
```

<210> 105
<211> 1650
<212> DNA
<213> Environmental

<400> 105

```
atgtccctat tcaaaaaaat ctttccgtgg attgtatctc tacttctttt gttttcgttt      60
attgctcctt tttccattca aacagaaaaa gtccgcgctg gaagtgttcc agtgaatgga     120
acgatgatgc aatatttcga atggtacctt ccagacgatg gaacactatg gacgaaagta     180
gcaaataacg cccaatcttt agcgaatctt ggcattactg ccctttggct tccccctgcc     240
tataaaggaa caagcagcag tgacgttgga tatggcgttt atgatttata tgacctagga     300
gagtttaatc aaaaaggaac tgtccgaaca aaatacggaa caaaaacaca atatatccaa     360
gcaatccaag cggcgcatac agcaggaatg caagtatatg cagatgtcgt ctttaaccat     420
aaagccggtg cagatgggac agaactagtg gatgcagtag aagtaaaccc ttctgaccgc     480
aatcaagaaa tatcaggaac atatcaaatc caagcgtgga caaaatttga ttttcctggt     540
cgtggaaaca cctattctag ttttaaatgg cgttggtatc atttcgatgg aacggactgg     600
gatgagagta gaaaactaaa tcgtatttac aaattccgcg gcacgggaaa agcatgggat     660
tgggaagtag atacagaaaa tgggaattat gactatctca tgtatgcaga tttggatatg     720
gatcatccag aggttgtatc tgaactaaaa aattggggaa agtggtatgt aaccacaacc     780
aatatcgacg gattccgtct ggatgcagtg aagcatatta aatatagctt tttcccagac     840
tggctatcgt atgtacgaac ccaaacacaa aagcctcttt ttgccgttgg cgaattttgg     900
agctatgaca ttaacaagct acacaactat attacaaaga cgaacggctc tatgtcccta     960
ttcgatgccc cgctgcataa caatttttat atagcatcga aatcaggtgg ctattttgat    1020
atgcgcacat tactcaacaa cacattgatg aaagatcaac caacactatc ggtcacatta    1080
gtagacaatc acgatactga gccagggcaa tctttgcagt cgtgggtcga gccgtggttt    1140
aaaccgttag cttacgcatt tatcttgacc cgccaagaag gttatccgtg catcttttat    1200
ggagattact atggtattcc aaaatacaac attcctgcgc tgaaaagcaa acttgatccg    1260
ctgttaattg ctcgaagaga ttatgcctac ggaacacagc acgactatat tgacaatgca    1320
gatattatcg gctggacgcg ggaaggagta gctgaaaaag caaattcggg acttgctgca    1380
ctcattaccg acggacctgg cggaagcaaa tggatgtatg ttggcaaaca acacgctggc    1440
aaaacgtttt atgatctaac cggcaatcga agtgatacag tgacaatcaa cgctgatgga    1500
tggggagaat ttaaagtcaa tggagggtct gtatccatat gggttccaaa aacatcaacc    1560
acttcccaaa tcacatttac tgtaaataat gccacaaccg tttggggaca aaatgtatac    1620
gttgtcggga atatttcgca gctgggcaac                                     1650
```

<210> 106
<211> 550
<212> PRT
<213> Environmental

<400> 106

```
Met Ser Leu Phe Lys Lys Ile Phe Pro Trp Ile Val Ser Leu Leu Leu
 1               5                  10                  15
Leu Phe Ser Phe Ile Ala Pro Phe Ser Ile Gln Thr Glu Lys Val Arg
            20                  25                  30
Ala Gly Ser Val Pro Val Asn Gly Thr Met Met Gln Tyr Phe Glu Trp
        35                  40                  45
Tyr Leu Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Asn Ala
    50                  55                  60
Gln Ser Leu Ala Asn Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala
65                  70                  75                  80
Tyr Lys Gly Thr Ser Ser Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu
```

```
                85                  90                  95
Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr
            100                 105                 110
Gly Thr Lys Thr Gln Tyr Ile Gln Ala Ile Gln Ala Ala His Thr Ala
        115                 120                 125
Gly Met Gln Val Tyr Ala Asp Val Val Phe Asn His Lys Ala Gly Ala
    130                 135                 140
Asp Gly Thr Glu Leu Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg
145                 150                 155                 160
Asn Gln Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe
                165                 170                 175
Asp Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp
            180                 185                 190
Tyr His Phe Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg
        195                 200                 205
Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
    210                 215                 220
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met
225                 230                 235                 240
Asp His Pro Glu Val Val Ser Glu Leu Lys Asn Trp Gly Lys Trp Tyr
                245                 250                 255
Val Thr Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His
            260                 265                 270
Ile Lys Tyr Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Thr Gln
        275                 280                 285
Thr Gln Lys Pro Leu Phe Ala Val Gly Glu Phe Trp Ser Tyr Asp Ile
    290                 295                 300
Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asn Gly Ser Met Ser Leu
305                 310                 315                 320
Phe Asp Ala Pro Leu His Asn Asn Phe Tyr Ile Ala Ser Lys Ser Gly
                325                 330                 335
Gly Tyr Phe Asp Met Arg Thr Leu Leu Asn Asn Thr Leu Met Lys Asp
            340                 345                 350
Gln Pro Thr Leu Ser Val Thr Leu Val Asp Asn His Asp Thr Glu Pro
        355                 360                 365
Gly Gln Ser Leu Gln Ser Trp Val Glu Pro Trp Phe Lys Pro Leu Ala
    370                 375                 380
Tyr Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Ile Phe Tyr
385                 390                 395                 400
Gly Asp Tyr Tyr Gly Ile Pro Lys Tyr Asn Ile Pro Ala Leu Lys Ser
                405                 410                 415
Lys Leu Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr
            420                 425                 430
Gln His Asp Tyr Ile Asp Asn Ala Asp Ile Ile Gly Trp Thr Arg Glu
        435                 440                 445
Gly Val Ala Glu Lys Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp
    450                 455                 460
Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly
465                 470                 475                 480
Lys Thr Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile
                485                 490                 495
Asn Ala Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser
            500                 505                 510
Ile Trp Val Pro Lys Thr Ser Thr Thr Ser Gln Ile Thr Phe Thr Val
        515                 520                 525
Asn Asn Ala Thr Thr Val Trp Gly Gln Asn Val Tyr Val Val Gly Asn
    530                 535                 540
```

```
Ile Ser Gln Leu Gly Asn
545                 550

<210> 107
<211> 1509
<212> DNA
<213> Environmental

<400> 107
atggacagcc tcgacgcgcc ggagcagaag ccctgggtga aggatggcag gctctccgcg      60
tacctggata cagggacagg gaccgtggtc gctcccgagg cacctgcgcc cccgccgccc     120
ccggccgagg aagtccggcc cgtggacaag tggaaaaacg atatcatcta tttcgtcctc     180
accgaccgtt tccaggatgg cgacaagacc aacaacatgg acgtggtccc gacggacatg     240
aaaaaatatc atggcggcga catccagggg ctcatcgaca agctcgacta tatcaaggag     300
accggttcga cggccatctg gctcacgccc cctatgaagg ggcagaccca cttcttcgag     360
accgacaatt accatggtta ctggcccatt gacttctatg acacggaccc ccatgtgggc     420
accatgcaga aatttgagga gcttatcgag aaagcccatg agaaagggct gaagatcgtg     480
ctcgatattc ccctgaacca cacggcctgg gagcatccct tctacaagga cgacagcaag     540
aaggactggt tccaccatat aggagatgtg aaggactggg aagatcccta ctgggctgaa     600
aacggctcca tattcggtct tcctgacctg gcgcaggaaa accctgccgt ggaaaagtac     660
ctcatcgacg tggccaagtt ctgggtagac aagggtattg acggcttcag gcttgacgcc     720
gtgaagaacg tgcccctcaa cttctgggcg aagtttgacc gggcgattca cgattatgcg     780
ggcaaggact tcctcctcgt cggggaatac tttgacggaa acccggcgaa agtcgcgaac     840
taccagagag aggacatgag ctcactcttc gattacccgc tctactggac cctgaaggac     900
accttcgcca aggacgggag catgcgcaac ctggcggcga agcttgatga gtgcgacagg     960
aattatcccg acccgggcct catgtcggtt ttccttgata accacgacac gccgaggttc    1020
ctcaccgagg ccaacggcaa caaggataag ctcaaactgg ccctcgcctt cgcgatgacc    1080
atcaaccgca tgcctaccat ttattatggc accgaggttg ccatggaagg caactgcgat    1140
atcatgggcg ccgtagataa ccggagggac atgcagtggg acaaggatcc tgacatgttc    1200
aaatacttca agactctcac cactgcccgc aatgagcatg aatccctcag ggaaggaaag    1260
aagctcgaga tgtggcagga tgacaaagtc tacgcgtacg ggaggcagac cccgaaggac    1320
gagtctatcg tggtgcttaa caacggctat gatacgcagg aacgggacat accgctccgc    1380
cccgagagcg gcatcaagaa cggcacggtg ctgaaggatg tcatcaccgg cgaaaccgtg    1440
acggtacaga acggaaaaat ccatgcgaaa tgcggcggca aacaggcgcg gatctacgtg    1500
cccgcgtag                                                           1509

<210> 108
<211> 502
<212> PRT
<213> Environmental

<400> 108
Met Asp Ser Leu Asp Ala Pro Glu Gln Lys Pro Trp Val Lys Asp Gly
 1               5                  10                  15
Arg Leu Ser Ala Tyr Leu Asp Thr Gly Thr Gly Thr Val Val Ala Pro
            20                  25                  30
Glu Ala Pro Ala Pro Pro Pro Pro Pro Ala Glu Glu Val Arg Pro Val
        35                  40                  45
Asp Lys Trp Lys Asn Asp Ile Ile Tyr Phe Val Leu Thr Asp Arg Phe
    50                  55                  60
Gln Asp Gly Asp Lys Thr Asn Asn Met Asp Val Val Pro Thr Asp Met
65                  70                  75                  80
Lys Lys Tyr His Gly Gly Asp Ile Gln Gly Leu Ile Asp Lys Leu Asp
                85                  90                  95
Tyr Ile Lys Glu Thr Gly Ser Thr Ala Ile Trp Leu Thr Pro Pro Met
            100                 105                 110
Lys Gly Gln Thr His Phe Phe Glu Thr Asp Asn Tyr His Gly Tyr Trp
```

```
        115                 120                 125
Pro Ile Asp Phe Tyr Asp Thr Asp Pro His Val Gly Thr Met Gln Lys
    130                 135                 140
Phe Glu Glu Leu Ile Glu Lys Ala His Glu Lys Gly Leu Lys Ile Val
145                 150                 155                 160
Leu Asp Ile Pro Leu Asn His Thr Ala Trp Glu His Pro Phe Tyr Lys
                165                 170                 175
Asp Asp Ser Lys Lys Asp Trp Phe His His Ile Gly Asp Val Lys Asp
            180                 185                 190
Trp Glu Asp Pro Tyr Trp Ala Glu Asn Gly Ser Ile Phe Gly Leu Pro
        195                 200                 205
Asp Leu Ala Gln Glu Asn Pro Ala Val Glu Lys Tyr Leu Ile Asp Val
    210                 215                 220
Ala Lys Phe Trp Val Asp Lys Gly Ile Asp Gly Phe Arg Leu Asp Ala
225                 230                 235                 240
Val Lys Asn Val Pro Leu Asn Phe Trp Ala Lys Phe Asp Arg Ala Ile
                245                 250                 255
His Asp Tyr Ala Gly Lys Asp Phe Leu Leu Val Gly Glu Tyr Phe Asp
            260                 265                 270
Gly Asn Pro Ala Lys Val Ala Asn Tyr Gln Arg Glu Asp Met Ser Ser
        275                 280                 285
Leu Phe Asp Tyr Pro Leu Tyr Trp Thr Leu Lys Asp Thr Phe Ala Lys
    290                 295                 300
Asp Gly Ser Met Arg Asn Leu Ala Ala Lys Leu Asp Glu Cys Asp Arg
305                 310                 315                 320
Asn Tyr Pro Asp Pro Gly Leu Met Ser Val Phe Leu Asp Asn His Asp
                325                 330                 335
Thr Pro Arg Phe Leu Thr Glu Ala Asn Gly Asn Lys Asp Lys Leu Lys
            340                 345                 350
Leu Ala Leu Ala Phe Ala Met Thr Ile Asn Arg Met Pro Thr Ile Tyr
        355                 360                 365
Tyr Gly Thr Glu Val Ala Met Glu Gly Asn Cys Asp Ile Met Gly Ala
    370                 375                 380
Val Asp Asn Arg Arg Asp Met Gln Trp Asp Lys Asp Pro Asp Met Phe
385                 390                 395                 400
Lys Tyr Phe Lys Thr Leu Thr Thr Ala Arg Asn Glu His Glu Ser Leu
                405                 410                 415
Arg Glu Gly Lys Lys Leu Glu Met Trp Gln Asp Asp Lys Val Tyr Ala
            420                 425                 430
Tyr Gly Arg Gln Thr Pro Lys Asp Glu Ser Ile Val Val Leu Asn Asn
        435                 440                 445
Gly Tyr Asp Thr Gln Glu Arg Asp Ile Pro Leu Arg Pro Glu Ser Gly
    450                 455                 460
Ile Lys Asn Gly Thr Val Leu Lys Asp Val Ile Thr Gly Glu Thr Val
465                 470                 475                 480
Thr Val Gln Asn Gly Lys Ile His Ala Lys Cys Gly Gly Lys Gln Ala
                485                 490                 495
Arg Ile Tyr Val Pro Ala
            500
```

<210> 109
<211> 1374
<212> DNA
<213> Environmental

<400> 109
atggcaagaa aaacgctggc catatttttc gtacttctag tgcttcttag tctctcggca 60

```
gttccggcaa aggcagaaac tctagagaat ggtggagtta taatgcaggc tttctattgg     120
gatgttcctg gaggaggaat ctggtgggac acaatagctc aaaagatacc cgaatgggca     180
agtgcaggaa tctcagcgat atggattcca ccagcgagta agggcatgag cggtggttat     240
tccatgggct acgatcccta cgatttcttt gacctcggcg agtactatca gaaggggaca     300
gttgagacgc gcttcggctc aaaggaagaa ctggtgaaca tgataaacac cgcacactcc     360
tacggcataa aggtgatagc ggacatagtc ataaaccacc gcgccggtgg agaccttgag     420
tggaacccct tcgtgaacga ctatacctgg acagacttct caaaagtcgc ctccggtaaa     480
tatacggcca actaccttga cttccaccca aacgagcttc actgttgtga tgaaggtacc     540
tttggaggat accctgatat atgtcacgac aaaagctggg accagtactg gctctgggcg     600
agcagcgaaa gctacgctgc ctacctcagg agcatagggg ttgacgcctg gcgtttcgac     660
tacgtcaagg gctacggagc atgggttgtt aacgactggc tcagctggtg gggaggctgg     720
gccgttggag agtactggga cacgaacgtt gatgcactcc tcaactgggc atacagcagc     780
ggcgccaagg tctttgactt cccgctctac tacaagatgg acgaagcctt cgacaacacc     840
aacatcccgg cattagtgga tgcactcaga tacggccaga cagtggtcag ccgcgatccc     900
ttcaaggcgg taactttcgt tgccaaccac gatacagata taatctggaa caagtatccg     960
gcttatgcat tcatccttac ctatgaggga cagcctgtta tattctaccg cgactacgag    1020
gagtggctca acaaggataa gcttaacaac ctcatctgga tacacgatca ccttgctgga    1080
gggagtactg acattgttta ctacgacagc gacgagctta tctttgtgag aaacggctat    1140
ggcaccaaac caggactgat aacctatatc aacctcggct caagcaaagt tggaaggtgg    1200
gtctacgttc caaagttcgc cggttcatgc atccacgagt acaccggcaa cctcggcggt    1260
tggatagaca agtacgtctc ctccagcggc tgggtctatc ttgaggcccc agcccacgac    1320
ccggcgaacg gctactacgg ctactctgtc tggagctact gcggtgtggg ttga          1374

<210> 110
<211> 457
<212> PRT
<213> Environmental

<400> 110
Met Ala Arg Lys Thr Leu Ala Ile Phe Phe Val Leu Leu Val Leu Leu
 1               5                  10                  15
Ser Leu Ser Ala Val Pro Ala Lys Ala Glu Thr Leu Glu Asn Gly Gly
            20                  25                  30
Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Gly Gly Gly Ile Trp
        35                  40                  45
Trp Asp Thr Ile Ala Gln Lys Ile Pro Glu Trp Ala Ser Ala Gly Ile
    50                  55                  60
Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr
65                  70                  75                  80
Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Tyr
                85                  90                  95
Gln Lys Gly Thr Val Glu Thr Arg Phe Gly Ser Lys Glu Glu Leu Val
            100                 105                 110
Asn Met Ile Asn Thr Ala His Ser Tyr Gly Ile Lys Val Ile Ala Asp
        115                 120                 125
Ile Val Ile Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe
    130                 135                 140
Val Asn Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys
145                 150                 155                 160
Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Cys Cys
                165                 170                 175
Asp Glu Gly Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser
            180                 185                 190
Trp Asp Gln Tyr Trp Leu Trp Ala Ser Ser Glu Ser Tyr Ala Ala Tyr
        195                 200                 205
Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly
    210                 215                 220
```

```
Tyr Gly Ala Trp Val Val Asn Asp Trp Leu Ser Trp Trp Gly Gly Trp
225                 230                 235                 240
Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp
                245                 250                 255
Ala Tyr Ser Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys
            260                 265                 270
Met Asp Glu Ala Phe Asp Asn Thr Asn Ile Pro Ala Leu Val Asp Ala
        275                 280                 285
Leu Arg Tyr Gly Gln Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val
    290                 295                 300
Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro
305                 310                 315                 320
Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro Val Ile Phe Tyr
                325                 330                 335
Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Lys Leu Asn Asn Leu Ile
            340                 345                 350
Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr
        355                 360                 365
Asp Ser Asp Glu Leu Ile Phe Val Arg Asn Gly Tyr Gly Thr Lys Pro
    370                 375                 380
Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp
385                 390                 395                 400
Val Tyr Val Pro Lys Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly
                405                 410                 415
Asn Leu Gly Gly Trp Ile Asp Lys Tyr Val Ser Ser Ser Gly Trp Val
            420                 425                 430
Tyr Leu Glu Ala Pro Ala His Asp Pro Ala Asn Gly Tyr Tyr Gly Tyr
        435                 440                 445
Ser Val Trp Ser Tyr Cys Gly Val Gly
    450                 455
```

<210> 111
<211> 1416
<212> DNA
<213> Environmental

<400> 111

```
atgcccgcgt tcaaatctaa ggtgatgcac atgaagttga agtaccttgc tttagttttg      60
ttggctgtgg cttcgatagg cctcctctcg actccagtgg gtgctgccaa gtactccgaa     120
ctcgaagagg gcggtgttat aatgcaggcc ttctactggg acgtccctac cggtgggatc     180
tggtgggaca ccataagaca gaaaatcccg gagtggtacg acgctggaat ctcggcgata     240
tggattcctc cagctagcaa aggtatgggt ggtgcatact ccatgggtta tgacccctac     300
gatttctttg acctcggcga gtactatcag aagggaacag ttgagacgcg cttcggctca     360
aaggaggaac tggtgaacat gataaacacc gcacactcct atggcataaa ggtgatagcg     420
gacatagtca taaaccaccg cgccggcggc gacctggagt ggaacccctt tgtaaacaac     480
tatacttgga cagacttctc caaggtcgcc tccggtaaat acacggccaa ctaccttgac     540
ttccacccaa acgaggtcaa gtgctgcgat gagggtacat ttggtgactt tccggacatc     600
gcccacgaga agagctggga tcagtactgg ctctgggcaa gcaatgagag ctacgccgcc     660
tatctccgga gcatagggat cgatgcatgg cgtttcgact acgtcaaagg ttacggagcg     720
tgggttgtta acgactggct cagctggtgg ggaggttggg ccgttggaga gtactgggac     780
accaacgttg atgcactcct taactgggca tacaacagcg gtgccaaggt ctttgacttc     840
ccgctctact acaagatgga cgaagccttt gacaacacca acatccccgc tttggtttac     900
gccctccaga acggaggaac agtcgtttcc cgcgatccct tcaaggcagt aactttcgtt     960
gccaaccacg ataccgatat aatctggaac aagtatccgg cttatgcgtt catccttacc    1020
tatgagggac agcctgttat attctaccgc gactacgagg agtggctcaa caaggataag    1080
cttaacaacc ttatctggat acacgagcac cttgccggag gaagtaccaa gatcctctac    1140
tacgataacg atgagctaat attcatgagg gagggctacg ggagcaagcc gggcctcata    1200
```

```
acctacataa acctcggaaa cgactgggcc gagcgctggg tgaacgtcgg ctcaaagttt    1260
gccggctaca caatccatga atacacaggc aatctcggtg gctgggttga caggtgggtt    1320
cagtacgacg gatgggttaa actgacggca cctcctcacg atccagccaa cggatattac    1380
ggctactcag tctggagcta cgcaggcgtc ggatga                              1416

<210> 112
<211> 471
<212> PRT
<213> Environmental

<400> 112
Met Pro Ala Phe Lys Ser Lys Val Met His Met Lys Leu Lys Tyr Leu
 1               5                  10                  15
Ala Leu Val Leu Leu Ala Val Ala Ser Ile Gly Leu Leu Ser Thr Pro
            20                  25                  30
Val Gly Ala Ala Lys Tyr Ser Glu Leu Glu Glu Gly Gly Val Ile Met
        35                  40                  45
Gln Ala Phe Tyr Trp Asp Val Pro Thr Gly Gly Ile Trp Trp Asp Thr
    50                  55                  60
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
65                  70                  75                  80
Trp Ile Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly
                85                  90                  95
Tyr Asp Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
            100                 105                 110
Thr Val Glu Thr Arg Phe Gly Ser Lys Glu Glu Leu Val Asn Met Ile
        115                 120                 125
Asn Thr Ala His Ser Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
    130                 135                 140
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asn
145                 150                 155                 160
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
                165                 170                 175
Asn Tyr Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly
            180                 185                 190
Thr Phe Gly Asp Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln
        195                 200                 205
Tyr Trp Leu Trp Ala Ser Asn Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
    210                 215                 220
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
225                 230                 235                 240
Trp Val Val Asn Asp Trp Leu Ser Trp Trp Gly Gly Trp Ala Val Gly
                245                 250                 255
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Asn
            260                 265                 270
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu
        275                 280                 285
Ala Phe Asp Asn Thr Asn Ile Pro Ala Leu Val Tyr Ala Leu Gln Asn
    290                 295                 300
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
305                 310                 315                 320
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
                325                 330                 335
Phe Ile Leu Thr Tyr Glu Gly Gln Pro Val Ile Phe Tyr Arg Asp Tyr
            340                 345                 350
Glu Glu Trp Leu Asn Lys Asp Lys Leu Asn Asn Leu Ile Trp Ile His
        355                 360                 365
```

```
Glu His Leu Ala Gly Gly Ser Thr Lys Ile Leu Tyr Tyr Asp Asn Asp
    370                 375                 380
Glu Leu Ile Phe Met Arg Glu Gly Tyr Gly Ser Lys Pro Gly Leu Ile
385                 390                 395                 400
Thr Tyr Ile Asn Leu Gly Asn Asp Trp Ala Glu Arg Trp Val Asn Val
                405                 410                 415
Gly Ser Lys Phe Ala Gly Tyr Thr Ile His Glu Tyr Thr Gly Asn Leu
            420                 425                 430
Gly Gly Trp Val Asp Arg Trp Val Gln Tyr Asp Gly Trp Val Lys Leu
        435                 440                 445
Thr Ala Pro Pro His Asp Pro Ala Asn Gly Tyr Tyr Gly Tyr Ser Val
    450                 455                 460
Trp Ser Tyr Ala Gly Val Gly
465                 470
```

<210> 113
<211> 1539
<212> DNA
<213> Environmental

<400> 113

```
atgaaacaac aaaaacggct ttacgcccga ttgctgacgc tgttatttgc gctcatcttc      60
ttgctgcctc attctgcagc agcggcggca aatcttaatg ggacgctgat gcagtatttt     120
gaatggtaca tgcccaatga cggccaacat tggaagcgct tgcaaaacga ctcggcatat     180
ttggctgaac acggtattac tgccgtctgg attccccccgg catataaggg aacgagccaa     240
gcggatgtgg gctacggtgc ttacgacctt tatgatttag gggagtttca tcaaaaaggg     300
acggttcgga caaagtacgg cacaaaagga gagctgcaat ctgcgatcaa aagtcttcat     360
tcccgcgaca ttaacgttta cggggatgtg gtcatcaacc acaaaggcgg cgctgatgcg     420
accgaagatg taaccgcggt tgaagtcgat cccgctgacc gcaaccgcgt aatttcagga     480
gaacaccgaa ttaaagcctg gacacatttt cattttccgg ggcgcggcag cacatacagc     540
gattttaaat ggcattggta ccattttgac ggaaccgatt gggacgagtc ccgaaagctg     600
aaccgcatct ataagtttca aggaaaggct tgggattggg aagtttccaa tgaaaacggc     660
aactatgatt atttgatgta tgccgacatc gattatgacc atcctgatgt cgcagcagaa     720
attaagagat ggggcacttg gtatgccaat gaactgcaat tggacggttt ccgtcttgat     780
gctgtcaaac acattaaatt ttctttttttg cgggattggg ttaatcatgt cagggaaaaa     840
acggggaagg aaatgtttac ggtagctgaa tattggcaga atgacttggg cgcgctggaa     900
aactatttga acaaaacaaa ttttaatcat tcagtgtttg acgtgccgct tcattatcag     960
ttccatgctg catcgacaca gggaggcggc tatgatatga ggaaattgct gaacggtacg    1020
gtcgtttcca agcatccgtt gaaagcggtt acatttgtcg ataaccatga tacacagccg    1080
gggcaatcgc ttgagtcgac tgtccaaaca tggtttaagc cgcttgctta cgctttcatt    1140
ctcacaaggg aatctggata ccctcaggtt ttctacgggg atatgtacgg gacgaaagga    1200
gactcccagc gcgaaattcc tgccttgaaa cacaaaattg aaccgatctt aaaagcgaga    1260
aaacagtatg cgtacggagc acagcatgat tatttcgacc accatgacat tgtcggctgg    1320
acaagggaag gcgacagctc ggttgcaaat tcaggtttgg cggcattaat aacagacgga    1380
cccggtgggg caaagcgaat gtatgtcggc cggcaaaacg ccggtgagac atggcatgac    1440
attaccggaa accgttcgga gccggttgtc atcaattcgg aaggctgggg agagtttcac    1500
gtaaacggcg ggtcggtttc aatttatgtt caaagatag                           1539
```

<210> 114
<211> 512
<212> PRT
<213> Environmental

<400> 114

```
Met Lys Gln Gln Lys Arg Leu Tyr Ala Arg Leu Leu Thr Leu Leu Phe
 1               5                  10                  15
Ala Leu Ile Phe Leu Leu Pro His Ser Ala Ala Ala Ala Ala Asn Leu
```

```
            20                  25                  30
Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro Asn Asp Gly
        35                  40                  45
Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu Ala Glu His
    50                  55                  60
Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln
65                  70                  75                  80
Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe
                85                  90                  95
His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu Leu
            100                 105                 110
Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr Gly
        115                 120                 125
Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp Val
    130                 135                 140
Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser Gly
145                 150                 155                 160
Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg Gly
                165                 170                 175
Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Thr
            180                 185                 190
Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln Gly
        195                 200                 205
Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp Tyr
    210                 215                 220
Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala Glu
225                 230                 235                 240
Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp Gly
                245                 250                 255
Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg Asp
            260                 265                 270
Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr Val
        275                 280                 285
Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu Asn
    290                 295                 300
Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr Gln
305                 310                 315                 320
Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys Leu
                325                 330                 335
Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr Phe
            340                 345                 350
Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr Val
        355                 360                 365
Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Glu
    370                 375                 380
Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys Gly
385                 390                 395                 400
Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro Ile
                405                 410                 415
Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr Phe
            420                 425                 430
Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser Val
        435                 440                 445
Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ala
    450                 455                 460
Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His Asp
465                 470                 475                 480
```

```
Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly Trp
                485                 490                 495
Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln Arg
            500                 505                 510
```

<210> 115
<211> 1338
<212> DNA
<213> Eukaryote

<400> 115

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atggcgaagt actccgagct ggagcagggc ggagtcataa tgcaggcctt ctactgggac      60
gttccggagg gaggaatctg gtgggacaca atacggcaga agatccctga atggtacgat     120
gcaggcatat ccgccatctg gataccccg gcgagcaagg gcatgggcgg ggcctactcg      180
atgggctacg acccctacga ttacttcgat ctgggcgagt tttaccagaa gggaaccgtt     240
gagacccgct tcggctccaa ggaagagctc gtcaacatga tctccacggc ccaccagtac     300
ggcatcaagg ttatagcgga catagtgata aaccaccgcg caggtggaga cctcgaatgg     360
aacccatacg tcggcgacta tacctggacg gacttttcta aggtcgcctc cgggaaatac     420
aaggcccact acatggactt ccatccaaac aactacagca cctcagacga gggaaccttc     480
ggtggcttcc cagacattga tcacctcgtg cccttcaacc agtactggct gtgggcgagc     540
aacgagagct acgccgccta cctcaggagc atagggatcg atgcgtggcg ctttgactac     600
gttaagggct acggcgcgtg ggtcgtcaag gactggctga gtcagtgggg cggctgggcc     660
gtcggcgagt actgggacac caacgtcgat gcgctcctca actgggccta cagcagcggc     720
gccaaggtct tcgacttccc gctctactac aagatggacg aggcctttga caacaagaac     780
attcccgccc tcgtttacgc catccagaac ggtgaaaccg tcgtcagcag ggatcccttc     840
aaggccgtta ccttcgtggc taaccacgat acgaacataa tctggaacaa gtaccctgcc     900
tatgccttca tcctgaccta cgaaggtcag cccgtcatct tctaccgcga ctacgaggag     960
tggctcaaca aggacaaact caacaacctc atatggattc acgagcacct ggcaggggga    1020
agcaccaaga tcctctacta cgacgacgat gagctcatct tcatgaggga aggctacggc    1080
gacaggcccg ggcttataac ctacatcaac ctcggtagcg actgggcgga gagatgggtg    1140
aacgttggct caaagttcgc gggctataca atccacgaat acaccggaaa cctcggcggc    1200
tgggtcgaca ggtacgtcca gtacgacggc tgggtcaagc ttaccgctcc gccacacgat    1260
ccggcaaacg gctattacgg ctactcggtc tggagctacg ccggagttgg aagatctcat    1320
caccatcacc atcactaa                                                  1338
```

<210> 116
<211> 445
<212> PRT
<213> Eukaryote

<400> 116

```
Met Ala Lys Tyr Ser Glu Leu Glu Gln Gly Gly Val Ile Met Gln Ala
 1               5                  10                  15
Phe Tyr Trp Asp Val Pro Glu Gly Gly Ile Trp Trp Asp Thr Ile Arg
            20                  25                  30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
        35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
    50                  55                  60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Phe Tyr Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Glu Glu Leu Val Asn Met Ile Ser Thr
                85                  90                  95
Ala His Gln Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
            100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Tyr Val Gly Asp Tyr Thr
        115                 120                 125
```

```
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Lys Ala His Tyr
    130                 135                 140
Met Asp Phe His Pro Asn Asn Tyr Ser Thr Ser Asp Glu Gly Thr Phe
145                 150                 155                 160
Gly Gly Phe Pro Asp Ile Asp His Leu Val Pro Phe Asn Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Asn Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
            180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
        195                 200                 205
Val Lys Asp Trp Leu Ser Gln Trp Gly Gly Trp Ala Val Gly Glu Tyr
    210                 215                 220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Tyr Ala Ile Gln Asn Gly Glu
            260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
        275                 280                 285
His Asp Thr Asn Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
    290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Asn Asn Leu Ile Trp Ile His Glu His
                325                 330                 335
Leu Ala Gly Gly Ser Thr Lys Ile Leu Tyr Tyr Asp Asp Asp Glu Leu
            340                 345                 350
Ile Phe Met Arg Glu Gly Tyr Gly Asp Arg Pro Gly Leu Ile Thr Tyr
        355                 360                 365
Ile Asn Leu Gly Ser Asp Trp Ala Glu Arg Trp Val Asn Val Gly Ser
    370                 375                 380
Lys Phe Ala Gly Tyr Thr Ile His Glu Tyr Thr Gly Asn Leu Gly Gly
385                 390                 395                 400
Trp Val Asp Arg Tyr Val Gln Tyr Asp Gly Trp Val Lys Leu Thr Ala
                405                 410                 415
Pro Pro His Asp Pro Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser
            420                 425                 430
Tyr Ala Gly Val Gly Arg Ser His His His His His His
        435                 440                 445
```

<210> 117
<211> 1476
<212> DNA
<213> Environmental

<400> 117

```
atgcgagtgt tcctggttgt gccaaagctg agccgcccat ttcaggcaga gtcacaacaa      60
caagacaggg acataacaat gaaacacaca gcgggaatgc tggcgatcgc aggtatgctg     120
atcgcccccc tggcgcatgc cgatgtcata ctgcacgcct tcaactggaa atacagtgaa     180
gtcaccgcca aggccgatct catcaaggct gccggctaca agcaggtgct catctcaccg     240
cctctgaagt cctcgggcaa cgagtggtgg gctcgttacc agccccagga tctgcgcctg     300
gtcgacaccc cccttggcaa caagcaggat ctggagcagc tgatcgccgc gatgcagacc     360
cggggcattg ccgtctacgc ggacgtggtg ctcaaccaca tggccaacga aagctggaag     420
cgcagcgacc tcaactaccc cggcagcgag ctgctgcaaa gctacgccgg caatccggcc     480
tactttgaac gccagaagct ctttggcgat ctggggcaga acttcctcgc cggccaggat     540
tttcatccgg aggggtgcat caccgactgg aacaatccgg gccatgtcca gtactggcga     600
```

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ctgtgcggcg gggcgggtga caaggggctg ccggatctgg accccaacaa ctgggtggtg     660
aaccagcaac aggcttacct gcaggcgctc aaggggatgg ggatcaaggg ttttcgggtc     720
gatgcggtca agcacatgag cgattaccag atcaacgccg tgttcacccc cgagatcaaa     780
caggggatgc acgtctttgg cgaggtgatc accacggggg gcgccggcaa cagcgactat     840
gagaacttcc tcaaacccta cctcgacagc agcggccagg gggcctacga cttcccgctc     900
ttcgcctccc tgcgtggagc gctgggctac ggcggcagca tgaacctgct ggccgatccc     960
ggtgcctatg gtcaggcgct gccgggtagc cgcgccgtca ccttcgccat cacccacgac    1020
atccccacca acgacggttt ccgctaccag atcctcaacc agaccgacga gagactggcc    1080
tatgcctacc tgctcggtcg cgatggcggt tcgcctctgg tctactccga tcacggtgaa    1140
accagggaca aggacggatt gcgctggcag gactactatc tgcgcaccga tctcaaaggg    1200
atgatccgct tccataacac agtgcagggt caaccgatgc agctcatcgg cagtaacgac    1260
tgcttcgtgc tgttcaagcg tggcaagcag ggcgtggtcg gcatcaacaa gtgcgactac    1320
gagcaggagt actggctcga taccgccaga ttcgagatga actggtatcg caactaccgg    1380
gatgtgctcg accagaatgc cgtggtcaac gtgcagagcc agtgggtaag gctgaccatc    1440
ccggcccgcg gcgccagaat gtggctgcag gagtga                               1476

<210> 118
<211> 491
<212> PRT
<213> Environmental

<400> 118
Met Arg Val Phe Leu Val Val Pro Lys Leu Ser Arg Pro Phe Gln Ala
 1               5                  10                  15
Glu Ser Gln Gln Gln Asp Arg Asp Ile Thr Met Lys His Thr Ala Gly
            20                  25                  30
Met Leu Ala Ile Ala Gly Met Leu Ile Ala Pro Leu Ala His Ala Asp
        35                  40                  45
Val Ile Leu His Ala Phe Asn Trp Lys Tyr Ser Glu Val Thr Ala Lys
    50                  55                  60
Ala Asp Leu Ile Lys Ala Ala Gly Tyr Lys Gln Val Leu Ile Ser Pro
65                  70                  75                  80
Pro Leu Lys Ser Ser Gly Asn Glu Trp Trp Ala Arg Tyr Gln Pro Gln
                85                  90                  95
Asp Leu Arg Leu Val Asp Thr Pro Leu Gly Asn Lys Gln Asp Leu Glu
            100                 105                 110
Gln Leu Ile Ala Ala Met Gln Thr Arg Gly Ile Ala Val Tyr Ala Asp
        115                 120                 125
Val Val Leu Asn His Met Ala Asn Glu Ser Trp Lys Arg Ser Asp Leu
    130                 135                 140
Asn Tyr Pro Gly Ser Glu Leu Leu Gln Ser Tyr Ala Gly Asn Pro Ala
145                 150                 155                 160
Tyr Phe Glu Arg Gln Lys Leu Phe Gly Asp Leu Gly Gln Asn Phe Leu
                165                 170                 175
Ala Gly Gln Asp Phe His Pro Glu Gly Cys Ile Thr Asp Trp Asn Asn
            180                 185                 190
Pro Gly His Val Gln Tyr Trp Arg Leu Cys Gly Gly Ala Gly Asp Lys
        195                 200                 205
Gly Leu Pro Asp Leu Asp Pro Asn Asn Trp Val Val Asn Gln Gln Gln
    210                 215                 220
Ala Tyr Leu Gln Ala Leu Lys Gly Met Gly Ile Lys Gly Phe Arg Val
225                 230                 235                 240
Asp Ala Val Lys His Met Ser Asp Tyr Gln Ile Asn Ala Val Phe Thr
                245                 250                 255
Pro Glu Ile Lys Gln Gly Met His Val Phe Gly Glu Val Ile Thr Thr
            260                 265                 270
Gly Gly Ala Gly Asn Ser Asp Tyr Glu Asn Phe Leu Lys Pro Tyr Leu
```

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        275                 280                 285
Asp Ser Ser Gly Gln Gly Ala Tyr Asp Phe Pro Leu Phe Ala Ser Leu
    290                 295                 300
Arg Gly Ala Leu Gly Tyr Gly Gly Ser Met Asn Leu Leu Ala Asp Pro
305                 310                 315                 320
Gly Ala Tyr Gly Gln Ala Leu Pro Gly Ser Arg Ala Val Thr Phe Ala
                325                 330                 335
Ile Thr His Asp Ile Pro Thr Asn Asp Gly Phe Arg Tyr Gln Ile Leu
            340                 345                 350
Asn Gln Thr Asp Glu Arg Leu Ala Tyr Ala Tyr Leu Leu Gly Arg Asp
        355                 360                 365
Gly Gly Ser Pro Leu Val Tyr Ser Asp His Gly Glu Thr Arg Asp Lys
    370                 375                 380
Asp Gly Leu Arg Trp Gln Asp Tyr Tyr Leu Arg Thr Asp Leu Lys Gly
385                 390                 395                 400
Met Ile Arg Phe His Asn Thr Val Gln Gly Gln Pro Met Gln Leu Ile
                405                 410                 415
Gly Ser Asn Asp Cys Phe Val Leu Phe Lys Arg Gly Lys Gln Gly Val
            420                 425                 430
Val Gly Ile Asn Lys Cys Asp Tyr Glu Gln Glu Tyr Trp Leu Asp Thr
        435                 440                 445
Ala Arg Phe Glu Met Asn Trp Tyr Arg Asn Tyr Arg Asp Val Leu Asp
    450                 455                 460
Gln Asn Ala Val Val Asn Val Gln Ser Gln Trp Val Arg Leu Thr Ile
465                 470                 475                 480
Pro Ala Arg Gly Ala Arg Met Trp Leu Gln Glu
                485                 490
```

<210> 119
<211> 1695
<212> DNA
<213> Bacterial

<400> 119

```
atgcaaacgt ttgcattctt attttactca aagaaaggat gggtgtgcat gaattatttg      60
aaaaaagtgt ggttgtatta cgctatcgtc gctaccttaa tcatttcctt tcttacacct     120
ttttcaacag cacaagctaa tactgcacct gttaacggaa caatgatgca atatttcgaa     180
tgggacttac ctaatgatgg gacgctttgg acgaaagtaa aaaatgaagc taccaatctt     240
tcttcactag gtatcacagc actatggctc cctccagcat ataaaggaac gagccaaagc     300
gatgtcggat acggtgttta cgatttatat gaccttgggg aatttaatca aaaagggacg     360
atccgaacga aatacggaac aaaaacacaa tatattcaag ccattcaaac tgcccaagcc     420
gcagggatgc aagtatatgc ggatgttgta tttaatcata aggcaggggc tgacagtaca     480
gaatttgtcg atgcagttga ggtaaaccct tctaatcgaa atcaagaaac atctggcaca     540
tatcaaattc aagcatggac aaaatttgat tttcctggtc gtggaaacac atactccagc     600
ttcaaatggc gctggtacca ttttgatggt acggattggg acgaaagtcg taaattaaat     660
cgtatttaca aattccgcgg tacaggaaaa gcgtgggact gggaagtcga tacagaaaac     720
ggaaactatg attatttaat gttcgctgat ttagatatgg atcaccctga ggttgtgaca     780
gaattaaaaa actggggaac gtggtacgtc aatactacaa atatcgatgg attccgctta     840
gatgccgtaa aacatattaa atacagcttt ttccctgact ggctaacata tgtacgtaat     900
caaacaggaa aaaatttatt tgccgttggg gaattttgga gctatgacgt caataagctg     960
cataattaca ttacaaaaac aaatgggtcg atgtcattat ttgatgcacc cttgcataac    1020
aacttttata ccgcttccaa atcgagtgga tattttgaca tgcgttattt attgaataat    1080
acattaatga aagatcaacc ttcactcgct gtaacacttg tcgataacca cgacacgcaa    1140
ccagggcaat ctttacagtc atgggtcgaa ccttggttta aacagcttgc ttacgccttt    1200
attttaacaa gacaagaagg gtatccttgc gtattttacg gtgattatta tggaatccct    1260
aaatacaata tcccggggtt aaaaagtaaa atcgacccgc ttttaattgc tcgtcgtgat    1320
tacgcttatg gaacacaacg tgattacatt gatcatcaag acattatcgg atggacacga    1380
```

```
gaaggcattg atgcaaaacc gaactctgga ctggcggctt taattaccga cggtcctggt    1440
ggaagtaaat ggatgtatgt cggtaaaaag catgccggga aagtatttta tgatttaact    1500
ggaaatcgaa gtgacacagt aacgattaat gcggatggtt ggggagaatt taaagtaaac    1560
ggaggatccg tctcaatttg ggtggctaaa acgtcaaacg tcacatttac agtcaataac    1620
gccacaacaa caagcggaca aaacgtatat gttgtcggca acattccaga gctaggcaat    1680
tgtcgcacgg gttaa                                                     1695

<210> 120
<211> 564
<212> PRT
<213> Bacterial

<400> 120
Met Gln Thr Phe Ala Phe Leu Phe Tyr Ser Lys Lys Gly Trp Val Cys
 1               5                  10                  15
Met Asn Tyr Leu Lys Lys Val Trp Leu Tyr Tyr Ala Ile Val Ala Thr
            20                  25                  30
Leu Ile Ile Ser Phe Leu Thr Pro Phe Ser Thr Ala Gln Ala Asn Thr
        35                  40                  45
Ala Pro Val Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Asp Leu Pro
    50                  55                  60
Asn Asp Gly Thr Leu Trp Thr Lys Val Lys Asn Glu Ala Thr Asn Leu
65                  70                  75                  80
Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys Gly
                85                  90                  95
Thr Ser Gln Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp Leu
            100                 105                 110
Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly Thr Lys
        115                 120                 125
Thr Gln Tyr Ile Gln Ala Ile Gln Thr Ala Gln Ala Ala Gly Met Gln
    130                 135                 140
Val Tyr Ala Asp Val Val Phe Asn His Lys Ala Gly Ala Asp Ser Thr
145                 150                 155                 160
Glu Phe Val Asp Ala Val Glu Val Asn Pro Ser Asn Arg Asn Gln Glu
                165                 170                 175
Thr Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe Pro
            180                 185                 190
Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His Phe
        195                 200                 205
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
    210                 215                 220
Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu Asn
225                 230                 235                 240
Gly Asn Tyr Asp Tyr Leu Met Phe Ala Asp Leu Asp Met Asp His Pro
                245                 250                 255
Glu Val Val Thr Glu Leu Lys Asn Trp Gly Thr Trp Tyr Val Asn Thr
            260                 265                 270
Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Tyr
        275                 280                 285
Ser Phe Phe Pro Asp Trp Leu Thr Tyr Val Arg Asn Gln Thr Gly Lys
    290                 295                 300
Asn Leu Phe Ala Val Gly Glu Phe Trp Ser Tyr Asp Val Asn Lys Leu
305                 310                 315                 320
His Asn Tyr Ile Thr Lys Thr Asn Gly Ser Met Ser Leu Phe Asp Ala
                325                 330                 335
Pro Leu His Asn Asn Phe Tyr Thr Ala Ser Lys Ser Ser Gly Tyr Phe
            340                 345                 350
```

```
Asp Met Arg Tyr Leu Leu Asn Asn Thr Leu Met Lys Asp Gln Pro Ser
        355                 360                 365
Leu Ala Val Thr Leu Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser
    370                 375                 380
Leu Gln Ser Trp Val Glu Pro Trp Phe Lys Gln Leu Ala Tyr Ala Phe
385                 390                 395                 400
Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp Tyr
                405                 410                 415
Tyr Gly Ile Pro Lys Tyr Asn Ile Pro Gly Leu Lys Ser Lys Ile Asp
            420                 425                 430
Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln Arg Asp
        435                 440                 445
Tyr Ile Asp His Gln Asp Ile Ile Gly Trp Thr Arg Glu Gly Ile Asp
    450                 455                 460
Ala Lys Pro Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly
465                 470                 475                 480
Gly Ser Lys Trp Met Tyr Val Gly Lys Lys His Ala Gly Lys Val Phe
                485                 490                 495
Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ala Asp
            500                 505                 510
Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Ile Trp Val
        515                 520                 525
Ala Lys Thr Ser Asn Val Thr Phe Thr Val Asn Asn Ala Thr Thr Thr
    530                 535                 540
Ser Gly Gln Asn Val Tyr Val Val Gly Asn Ile Pro Glu Leu Gly Asn
545                 550                 555                 560
Cys Arg Thr Gly
```

<210> 121
<211> 1556
<212> DNA
<213> Environmental

<400> 121

```
atgctcgccc tgtcgctcgg cggctgcggc atcgacgcgg gcccgacagg ccctcgcgtc      60
gtggagccgc tgccgcagcg ccccacgctt ccgcaggagt accgcgccag cggccacgcg     120
gccgccggcg acgtgttcgt gcacctgttc gagtggaagt ggccggacat cgcggaggaa     180
tgcgagaacg tgctggggcc ggcgggctac gaggcggtgc aggtgtcgcc gccgcaggag     240
cacctggtgc agcaggggcc gccgtggtgg cagcggtacc agccggtgag ctactcggtg     300
gcgctgagcc gcagcggcac gggcgtggag ttcagcaaca tgatcagccg gtgcaaggcc     360
gccggcgtgg acatctacgt ggacgccgtc atcaaccaca tgacggccgg tgcggggacg     420
gggagcaacg gcaccgccta caccaagtac aactaccccg gcctgtacgc gcaggcggac     480
tttcacccgc agtgcgcggt gggcgactac accagcgccg ccaacgtgca ggactgcgaa     540
ctgctggggc tggctgacct gaacaccggc gcggccggcg tgcagcagaa gatcgcggac     600
tacctggtct cgctggcgcg gctgggcgtg gcgggttttc gcatcgacgc cgccaagcac     660
atccagccgg tggaactgga cgccatcgtg gaccgcgtga accagacgct ggcggcggag     720
gggcgcccgc ttccctactg gttcgccgag gtgatcgaca acggcggcga gggggtgcgg     780
cgcgagcact actacggcct gggatacggc accggcggcg ccgcggacat cacggagttc     840
cgctacaagg gcgtgggcga caagttcctg ggcagcggcg gccagcggct ggtggacctg     900
aagaacttct cggcggtgac gtggaacctg atgccgtcgg acaaggccgt cgtctttctg     960
gagaaccacg atacgcagcg cggcggcggc atcggctacc gcgatggcac ggcgttccgg    1020
ctggccaacg tgtggatgct ggcgcagccg tacggctatc cgtcggtgat gtccagctac    1080
gcctttgacc gcacctcccc ctttggccgc gacgccggcc cgccctccga ggacggcgcg    1140
acgaaggacg tgacgtgcgc gcccacgctg gagacggcgg tgctgggcac ctgggtgtgc    1200
gagcaccgcg accccgtcat tcagcggatg gtgggctttc gccgcgcgat ggcgggcacg    1260
gacctgaacc gctggtggga caacggcggc aacgccattg ccttttcgcg cggggaccgg    1320
```

```
ggcttcgtcg ccatcagccg cgagccgaag gtgaccatgg cggccgtgcc cagcggactg    1380
tcccccggca cctactgcga cgtgctgacc ggcggcaagg tgggcaacgc ctgcgcggga    1440
accagcgtga cggtcgactc tcagggcgtg gtgcagctga gcatcgtcga gaactcggct    1500
ctggtgatcc acctcggggc caagctgtaa cggcgcgctg gcggatgtgc ggaggg        1556

<210> 122
<211> 517
<212> PRT
<213> Environmental

<400> 122
Met Leu Ala Leu Ser Leu Gly Gly Cys Gly Ile Asp Ala Gly Pro Thr
 1               5                  10                  15
Gly Pro Arg Val Val Glu Pro Leu Pro Gln Arg Pro Thr Leu Pro Gln
            20                  25                  30
Glu Tyr Arg Ala Ser Gly His Ala Ala Ala Gly Asp Val Phe Val His
        35                  40                  45
Leu Phe Glu Trp Lys Trp Pro Asp Ile Ala Glu Glu Cys Glu Asn Val
    50                  55                  60
Leu Gly Pro Ala Gly Tyr Glu Ala Val Gln Val Ser Pro Pro Gln Glu
65                  70                  75                  80
His Leu Val Gln Gln Gly Ala Pro Trp Trp Gln Arg Tyr Gln Pro Val
                85                  90                  95
Ser Tyr Ser Val Ala Leu Ser Arg Ser Gly Thr Gly Val Glu Phe Ser
            100                 105                 110
Asn Met Ile Ser Arg Cys Lys Ala Ala Gly Val Asp Ile Tyr Val Asp
        115                 120                 125
Ala Val Ile Asn His Met Thr Ala Gly Ala Gly Thr Gly Ser Asn Gly
    130                 135                 140
Thr Ala Tyr Thr Lys Tyr Asn Tyr Pro Gly Leu Tyr Ala Gln Ala Asp
145                 150                 155                 160
Phe His Pro Gln Cys Ala Val Gly Asp Tyr Thr Ser Ala Ala Asn Val
                165                 170                 175
Gln Asp Cys Glu Leu Leu Gly Leu Ala Asp Leu Asn Thr Gly Ala Ala
            180                 185                 190
Gly Val Gln Gln Lys Ile Ala Asp Tyr Leu Val Ser Leu Ala Arg Leu
        195                 200                 205
Gly Val Ala Gly Phe Arg Ile Asp Ala Ala Lys His Ile Gln Pro Val
    210                 215                 220
Glu Leu Asp Ala Ile Val Asp Arg Val Asn Gln Thr Leu Ala Ala Glu
225                 230                 235                 240
Gly Arg Pro Leu Pro Tyr Trp Phe Ala Glu Val Ile Asp Asn Gly Gly
                245                 250                 255
Glu Gly Val Arg Arg Glu His Tyr Tyr Gly Leu Gly Tyr Gly Thr Gly
            260                 265                 270
Gly Ala Ala Asp Ile Thr Glu Phe Arg Tyr Lys Gly Val Gly Asp Lys
        275                 280                 285
Phe Leu Gly Ser Gly Gly Gln Arg Leu Val Asp Leu Lys Asn Phe Ser
    290                 295                 300
Ala Val Thr Trp Asn Leu Met Pro Ser Asp Lys Ala Val Val Phe Leu
305                 310                 315                 320
Glu Asn His Asp Thr Gln Arg Gly Gly Gly Ile Gly Tyr Arg Asp Gly
                325                 330                 335
Thr Ala Phe Arg Leu Ala Asn Val Trp Met Leu Ala Gln Pro Tyr Gly
            340                 345                 350
Tyr Pro Ser Val Met Ser Ser Tyr Ala Phe Asp Arg Thr Ser Pro Phe
        355                 360                 365
```

```
Gly Arg Asp Ala Gly Pro Pro Ser Glu Asp Gly Ala Thr Lys Asp Val
    370                 375                 380
Thr Cys Ala Pro Thr Leu Glu Thr Ala Val Leu Gly Thr Trp Val Cys
385                 390                 395                 400
Glu His Arg Asp Pro Val Ile Gln Arg Met Val Gly Phe Arg Arg Ala
                405                 410                 415
Met Ala Gly Thr Asp Leu Asn Arg Trp Trp Asp Asn Gly Gly Asn Ala
            420                 425                 430
Ile Ala Phe Ser Arg Gly Asp Arg Gly Phe Val Ala Ile Ser Arg Glu
        435                 440                 445
Pro Lys Val Thr Met Ala Ala Val Pro Ser Gly Leu Ser Pro Gly Thr
    450                 455                 460
Tyr Cys Asp Val Leu Thr Gly Gly Lys Val Gly Asn Ala Cys Ala Gly
465                 470                 475                 480
Thr Ser Val Thr Val Asp Ser Gln Gly Val Val Gln Leu Ser Ile Val
                485                 490                 495
Glu Asn Ser Ala Leu Val Ile His Leu Gly Ala Lys Leu Arg Arg Ala
            500                 505                 510
Gly Gly Cys Ala Glu
        515
```

<210> 123
<211> 1770
<212> DNA
<213> Environmental

<400> 123

```
atgccccagg ccattcgcac tttttcacgt tggacgttgt tcggcttaat cggcgttttt      60
ctgcttggtc tcgtcttttc tgtcccaccc cgggcaatcc aggcccagac aaccccggcc     120
cgtaccgtta tggttcacct cttcgagtgg aaatggaccg acatcgctaa agaatgcgag     180
aatttcctcg gaccgaaagg ctttgccgca atccaggtat cgccgcccca ggagcatgtc     240
caggggtcgc aatggtggac ccgctatcag ccggtcagct acaagatcga gagccgctcc     300
ggcacccggg ccgagttcgc caatatggtc tcgcgctgca aagccgtcgg ggtcgatatc     360
tatgtcgatg ccgtgatcaa ccatatgacg actgtcggct ccggcactgg tatggctgga     420
tcgacctaca ccagctacac ctatccgggg ctgtatcaga cccaggactt ccaccactgc     480
gggcgcaatg gcaacgatga tatcagcagc tacggcgatc gctgggaagt acaaaactgc     540
gaactgctca acctagccga cctcaacacc ggcgctgagt atgtccgggg taaactcgcc     600
gcctatatga acgatctgcg cggcctgggc gtcgccggat ttcggatcga tgccgccaag     660
cacatggata ccaacgacat caacaatatc gttggccgcc tgcccaacgc gccctacatc     720
taccaggaag tgatcgacca gggcggcgag ccaattaccg ccggcgaata cttccagaat     780
ggcgatgtga ccgagttcaa gtacagccgc gagatctcgc gcatgttcaa aaccggccag     840
ctgacccata tgagccagtt cggcactgcc tggggcttca tgtccagcga cctggcagta     900
gttttcaccg ataaccacga caaccagcgc ggtcacggcg gcgccggcga tgtcttgacc     960
tacaaagatg gccagctgta caccctgggc aatatcttcg agctagcctg gccgtatggc    1020
tacccacagg tcatgtcgag ctacacgttc agcaacggcg accaggggcc gccatcgacc    1080
aatgtgtacg caaccacaac gcctgattgt ggcaacggcc gctgggtctg tgagcaccgc    1140
tggcgaggaa tcgccaacat ggtcgcgttc cgcaactaca ccgccccgac cttcagcacc    1200
agcaactggt ggagcaacgg caacaaccag atcgctttca gccgcgggac cctgggcttt    1260
gtggcgatca atcgggaagg tggcagcctg aaccgcacct tccaaaccgg cctgcccgtc    1320
ggcacctact gcgatgtcat tcacggcgat ttcaatgcca gcgccggcac ctgttccggc    1380
ccaactatcg ctgtcaacgg ctccggacag gcaaccatca cggtcaacgc gatggacgcg    1440
gtggcgatct acggcggagc caggctcgcc actccggcca gtgtcaacgt gacattcaac    1500
gaaaacgcca cgaccacctg ggggcagaat gtgtatatcg tcggcaacgt cgccgccctg    1560
ggcagctgga acgcaggcag cgcggtctta ctctcctccg ctaactaccc aatctggagc    1620
aagaccatcg ccctgccagc caacaccgcc attgagtaca agtacatcaa aaaggatggc    1680
gcgggcaatg tggtgtggga aagcggcgcc aaccgcgtct ttaccacccc cggcagcggc    1740
agtgccacgc gcaacgatac ctggaaatag                                     1770
```

<210> 124
<211> 589
<212> PRT
<213> Environmental

<400> 124
Met Pro Gln Ala Ile Arg Thr Phe Ser Arg Trp Thr Leu Phe Gly Leu
 1   5   10   15
Ile Gly Val Phe Leu Leu Gly Leu Val Phe Ser Val Pro Pro Arg Ala
            20   25   30
Ile Gln Ala Gln Thr Thr Pro Ala Arg Thr Val Met Val His Leu Phe
        35   40   45
Glu Trp Lys Trp Thr Asp Ile Ala Lys Glu Cys Glu Asn Phe Leu Gly
    50   55   60
Pro Lys Gly Phe Ala Ala Ile Gln Val Ser Pro Pro Gln Glu His Val
65   70   75   80
Gln Gly Ser Gln Trp Trp Thr Arg Tyr Gln Pro Val Ser Tyr Lys Ile
                85   90   95
Glu Ser Arg Ser Gly Thr Arg Ala Glu Phe Ala Asn Met Val Ser Arg
            100   105   110
Cys Lys Ala Val Gly Val Asp Ile Tyr Val Asp Ala Val Ile Asn His
        115   120   125
Met Thr Thr Val Gly Ser Gly Thr Gly Met Ala Gly Ser Thr Tyr Thr
    130   135   140
Ser Tyr Thr Tyr Pro Gly Leu Tyr Gln Thr Gln Asp Phe His His Cys
145   150   155   160
Gly Arg Asn Gly Asn Asp Asp Ile Ser Ser Tyr Gly Asp Arg Trp Glu
                165   170   175
Val Gln Asn Cys Glu Leu Leu Asn Leu Ala Asp Leu Asn Thr Gly Ala
            180   185   190
Glu Tyr Val Arg Gly Lys Leu Ala Ala Tyr Met Asn Asp Leu Arg Gly
        195   200   205
Leu Gly Val Ala Gly Phe Arg Ile Asp Ala Ala Lys His Met Asp Thr
    210   215   220
Asn Asp Ile Asn Asn Ile Val Gly Arg Leu Pro Asn Ala Pro Tyr Ile
225   230   235   240
Tyr Gln Glu Val Ile Asp Gln Gly Gly Glu Pro Ile Thr Ala Gly Glu
                245   250   255
Tyr Phe Gln Asn Gly Asp Val Thr Glu Phe Lys Tyr Ser Arg Glu Ile
            260   265   270
Ser Arg Met Phe Lys Thr Gly Gln Leu Thr His Met Ser Gln Phe Gly
        275   280   285
Thr Ala Trp Gly Phe Met Ser Ser Asp Leu Ala Val Val Phe Thr Asp
    290   295   300
Asn His Asp Asn Gln Arg Gly His Gly Gly Ala Gly Asp Val Leu Thr
305   310   315   320
Tyr Lys Asp Gly Gln Leu Tyr Thr Leu Gly Asn Ile Phe Glu Leu Ala
                325   330   335
Trp Pro Tyr Gly Tyr Pro Gln Val Met Ser Ser Tyr Thr Phe Ser Asn
            340   345   350
Gly Asp Gln Gly Pro Pro Ser Thr Asn Val Tyr Ala Thr Thr Thr Pro
        355   360   365
Asp Cys Gly Asn Gly Arg Trp Val Cys Glu His Arg Trp Arg Gly Ile
    370   375   380
Ala Asn Met Val Ala Phe Arg Asn Tyr Thr Ala Pro Thr Phe Ser Thr
385   390   395   400

```
Ser Asn Trp Trp Ser Asn Gly Asn Asn Gln Ile Ala Phe Ser Arg Gly
                405                 410                 415
Thr Leu Gly Phe Val Ala Ile Asn Arg Glu Gly Gly Ser Leu Asn Arg
            420                 425                 430
Thr Phe Gln Thr Gly Leu Pro Val Gly Thr Tyr Cys Asp Val Ile His
        435                 440                 445
Gly Asp Phe Asn Ala Ser Ala Gly Thr Cys Ser Gly Pro Thr Ile Ala
    450                 455                 460
Val Asn Gly Ser Gly Gln Ala Thr Ile Thr Val Asn Ala Met Asp Ala
465                 470                 475                 480
Val Ala Ile Tyr Gly Gly Ala Arg Leu Ala Thr Pro Ala Ser Val Asn
                485                 490                 495
Val Thr Phe Asn Glu Asn Ala Thr Thr Thr Trp Gly Gln Asn Val Tyr
            500                 505                 510
Ile Val Gly Asn Val Ala Ala Leu Gly Ser Trp Asn Ala Gly Ser Ala
        515                 520                 525
Val Leu Leu Ser Ser Ala Asn Tyr Pro Ile Trp Ser Lys Thr Ile Ala
    530                 535                 540
Leu Pro Ala Asn Thr Ala Ile Glu Tyr Lys Tyr Ile Lys Lys Asp Gly
545                 550                 555                 560
Ala Gly Asn Val Val Trp Glu Ser Gly Ala Asn Arg Val Phe Thr Thr
                565                 570                 575
Pro Gly Ser Gly Ser Ala Thr Arg Asn Asp Thr Trp Lys
            580                 585
```

<210> 125
<211> 1395
<212> DNA
<213> Environmental

<400> 125

```
gtggtgcaca tgaagttgaa gtaccttgcc ttagttttgt tggctgtggc ttcgataggc      60
ctactctcga ctccagtggg tgctgccaag tactccgaac tcgaagaggg cggtgttata     120
atgcaggcct tctactggga tgttcccgga gggggaatct ggtgggacac cataagacag     180
aaaatcccgg agtggtacga cgctggaatc tcggcgatat ggattcctcc agctagcaaa     240
gggatgggcg gtggttattc catgggctac gatccctacg atttctttga cctcggcgag     300
tactatcaga agggaacagt tgagacgcgc ttcggctcaa aggaggaact ggtgaacatg     360
ataaacaccg cacactccta tggcataaag gtgatagcgg acatagtcat aaaccaccgc     420
gccggtggag accttgagtg gaaccccttt gtaaacaact atacttggac agacttctcc     480
aaggtcgcct ccggtaaata cacggccaac taccttgact tccacccaaa cgaggtcaag     540
tgctgcgatg agggtacatt tggtgacttt ccggacatcg cccacgagaa gagctgggat     600
cagtactggc tctgggcaag caatgagagc tacgccgcat atctccggag catagggatc     660
gatgcatggc gtttcgacta cgtcaaaggt tacggagcgt gggttgttaa tgactggctc     720
agctggtggg gaggctgggc cgttggagag tactgggaca cgaacgttga tgcactcctt     780
aactgggcat acgacagcgg tgccaaggtc tttgacttcc cgctctacta caagatggac     840
gaagcctttg acaacaccaa catccccgct ttggtttacg ccctccagaa cggaggaaca     900
gtcgtttccc gcgatccctt caaggcagta actttcgttg ccaaccacga tacagatata     960
atctggaaca agtatccggc ttatgcgttc atccttacct atgagggaca gcctgttata    1020
ttttaccgcg actacgagga gtggctcaac aaggataagc ttaacaacct tatctggata    1080
cacgagcacc ttgccggagg aagtaccaag atcctctact acgataacga tgagctaata    1140
ttcatgaggg agggctacgg gagcaagccg ggcctcataa cctacataaa cctcggaaac    1200
gactgggccg agcgctgggt gaacgtcggc tcaaagtttg ccggctacac aatccatgaa    1260
tacacaggca atctcggtgg ctgggttgac aggtgggttc agtacgatgg atgggttaaa    1320
ctgacggcac ctcctcatga tccagccaac ggatattacg gctactcagt ctggagctac    1380
gcaggcgtcg gatga                                                     1395
```

<210> 126

<211> 464
<212> PRT
<213> Environmental

<400> 126
Val Val His Met Lys Leu Lys Tyr Leu Ala Leu Val Leu Leu Ala Val
 1   5   10   15
Ala Ser Ile Gly Leu Leu Ser Thr Pro Val Gly Ala Ala Lys Tyr Ser
            20   25   30
Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val
        35   40   45
Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln Lys Ile Pro Glu
    50   55   60
Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys
65   70   75   80
Gly Met Gly Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe
                85   90   95
Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe Gly
            100   105   110
Ser Lys Glu Glu Leu Val Asn Met Ile Asn Thr Ala His Ser Tyr Gly
        115   120   125
Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp
    130   135   140
Leu Glu Trp Asn Pro Phe Val Asn Asn Tyr Thr Trp Thr Asp Phe Ser
145   150   155   160
Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro
                165   170   175
Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Asp Phe Pro Asp
            180   185   190
Ile Ala His Glu Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser Asn
        195   200   205
Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile Asp Ala Trp Arg
    210   215   220
Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Asn Asp Trp Leu
225   230   235   240
Ser Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val
                245   250   255
Asp Ala Leu Leu Asn Trp Ala Tyr Asp Ser Gly Ala Lys Val Phe Asp
            260   265   270
Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Thr Asn Ile
        275   280   285
Pro Ala Leu Val Tyr Ala Leu Gln Asn Gly Gly Thr Val Val Ser Arg
    290   295   300
Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile
305   310   315   320
Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly
                325   330   335
Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp
            340   345   350
Lys Leu Asn Asn Leu Ile Trp Ile His Glu His Leu Ala Gly Gly Ser
        355   360   365
Thr Lys Ile Leu Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Met Arg Glu
    370   375   380
Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Asn
385   390   395   400
Asp Trp Ala Glu Arg Trp Val Asn Val Gly Ser Lys Phe Ala Gly Tyr
                405   410   415

```
Thr Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Arg Trp
            420                 425                 430
Val Gln Tyr Asp Gly Trp Val Lys Leu Thr Ala Pro Pro His Asp Pro
        435                 440                 445
Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr Ala Gly Val Gly
    450                 455                 460
```

<210> 127
<211> 1848
<212> DNA
<213> Environmental

<400> 127

```
gtgtgcatga attatttgaa aaaagtgtgg ttgtattacg ctatcgtcgc taccttaatc      60
atttactttc ttacgccctt ttcaactgca caagccaaca ctgcaccagt caacggaacg     120
atgatgcaat atttcgaatg ggatttaccg aatgatggca cactttggac gaaagtaaaa     180
aacgaagcaa gcagtctttc ttctttaggt attactgcgt tatggttacc acctgcatac     240
aaaggaacga gccaagggga tgtcgggtat ggcgtgtacg atttgtatga cttaggagaa     300
tttaatcaaa aagggacgat tcgaacgaaa tacggaacaa aaacgcaata tttacaagcc     360
attcaagcgg caaaaagcgc tggcatgcaa gtatacgctg atgtcgtatt taatcacaag     420
gcgggggcag atagtacaga atgggttgac gcagtcgaag tgaatccttc taatcgaaac     480
caagaaacat ctggcacata tcaaattcaa gcatggacaa aatttgattt ccctggccgt     540
gggaacacat actcaagctt taaatggcga tggtatcatt ttgacggtac ggattgggat     600
gaaagccgaa aactaaatcg tatttacaaa tttcgtggca caggaaaagc atgggattgg     660
gaagtagaca cagagaacgg aaactatgac tacttaatgt ttgctgattt agatatggat     720
caccctgaag tcgtgacaga gctaaaaaac tggggaacat ggtacgtcaa tacgacaaat     780
gtcgatgggt ttcgcttaga tgcagtaaag catattaaat atagcttctt cccagattgg     840
ttaacacatg tgcgttcaca aacacgaaaa aatctttttg cagtaggaga attttggagc     900
tacgatgtca ataaactgca taactacatt acaaaaacaa gtggaaccat gtcgttattt     960
gatgcgccac ttcataacaa cttttacact gcttcaaaat ctagcgggta ttttgacatg    1020
cgctatttgt taaataatac gttgatgaaa gaccagcctt ctcttgcggt cacactcgtt    1080
gataatcatg acacgcaacc gggacaatct ttacaatcat gggtagagcc ttggtttaag    1140
ccgcttgctt atgcctttat tttgacaaga caagaaggat atccttgcgt attttacggc    1200
gactattacg gcatccctaa atacaacatt ccgggattga aaagtaaaat cgatccgctt    1260
ctcattgccc gtagagacta cgcatacgga acacaacgtg attatattga ccatcaagac    1320
attattggat ggacacggga aggaattgac tcaaaaccga actctggact tgcggcttta    1380
attactgacg gccctggtgg aagtaaatgg atgtatgtag gtaaaaagca tgctggaaaa    1440
gtgttttacg atctcactgg aaatcgaagc gatacggtaa cgattaatgc agacggctgg    1500
ggagagttta aagtaaacgg tggctccgtt tccatttggg ttgccaaaac atcacaagtc    1560
acgtttaccg tcaacaatgc gacaacgata agcggacaaa atgtgtatgt cgttggtaac    1620
attccagagc tcggaaattg gaacacagca aacgcaatca aaatgacccc atcttcttat    1680
ccaacgtgga aagcaaccat tgctcttcca caaggaaaag ccattgaatt taaatttatt    1740
aaaaaagacc aatcgggaaa tgttgtttgg gaaagcattc caaaccgaac atacaccgtt    1800
ccatttttat caacaggctc atatacagct agttggaatg taccttaa                1848
```

<210> 128
<211> 615
<212> PRT
<213> Environmental

<400> 128

```
Val Cys Met Asn Tyr Leu Lys Lys Val Trp Leu Tyr Tyr Ala Ile Val
 1               5                  10                  15
Ala Thr Leu Ile Ile Tyr Phe Leu Thr Pro Phe Ser Thr Ala Gln Ala
            20                  25                  30
Asn Thr Ala Pro Val Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Asp
        35                  40                  45
```

```
Leu Pro Asn Asp Gly Thr Leu Trp Thr Lys Val Lys Asn Glu Ala Ser
    50                  55                  60
Ser Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr
65                  70                  75                  80
Lys Gly Thr Ser Gln Gly Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr
                85                  90                  95
Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly
            100                 105                 110
Thr Lys Thr Gln Tyr Leu Gln Ala Ile Gln Ala Ala Lys Ser Ala Gly
        115                 120                 125
Met Gln Val Tyr Ala Asp Val Val Phe Asn His Lys Ala Gly Ala Asp
    130                 135                 140
Ser Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asn Arg Asn
145                 150                 155                 160
Gln Glu Thr Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp
                165                 170                 175
Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr
            180                 185                 190
His Phe Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile
        195                 200                 205
Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp Thr
    210                 215                 220
Glu Asn Gly Asn Tyr Asp Tyr Leu Met Phe Ala Asp Leu Asp Met Asp
225                 230                 235                 240
His Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Thr Trp Tyr Val
                245                 250                 255
Asn Thr Thr Asn Val Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile
            260                 265                 270
Lys Tyr Ser Phe Phe Pro Asp Trp Leu Thr His Val Arg Ser Gln Thr
        275                 280                 285
Arg Lys Asn Leu Phe Ala Val Gly Glu Phe Trp Ser Tyr Asp Val Asn
    290                 295                 300
Lys Leu His Asn Tyr Ile Thr Lys Thr Ser Gly Thr Met Ser Leu Phe
305                 310                 315                 320
Asp Ala Pro Leu His Asn Asn Phe Tyr Thr Ala Ser Lys Ser Ser Gly
                325                 330                 335
Tyr Phe Asp Met Arg Tyr Leu Leu Asn Asn Thr Leu Met Lys Asp Gln
            340                 345                 350
Pro Ser Leu Ala Val Thr Leu Val Asp Asn His Asp Thr Gln Pro Gly
        355                 360                 365
Gln Ser Leu Gln Ser Trp Val Glu Pro Trp Phe Lys Pro Leu Ala Tyr
    370                 375                 380
Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly
385                 390                 395                 400
Asp Tyr Tyr Gly Ile Pro Lys Tyr Asn Ile Pro Gly Leu Lys Ser Lys
                405                 410                 415
Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln
            420                 425                 430
Arg Asp Tyr Ile Asp His Gln Asp Ile Ile Gly Trp Thr Arg Glu Gly
        435                 440                 445
Ile Asp Ser Lys Pro Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly
    450                 455                 460
Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Lys His Ala Gly Lys
465                 470                 475                 480
Val Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn
                485                 490                 495
Ala Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Ile
```

```
            500                 505                 510
Trp Val Ala Lys Thr Ser Gln Val Thr Phe Thr Val Asn Asn Ala Thr
        515                 520                 525
Thr Ile Ser Gly Gln Asn Val Tyr Val Val Gly Asn Ile Pro Glu Leu
    530                 535                 540
Gly Asn Trp Asn Thr Ala Asn Ala Ile Lys Met Thr Pro Ser Ser Tyr
545                 550                 555                 560
Pro Thr Trp Lys Ala Thr Ile Ala Leu Pro Gln Gly Lys Ala Ile Glu
                565                 570                 575
Phe Lys Phe Ile Lys Lys Asp Gln Ser Gly Asn Val Val Trp Glu Ser
            580                 585                 590
Ile Pro Asn Arg Thr Tyr Thr Val Pro Phe Leu Ser Thr Gly Ser Tyr
        595                 600                 605
Thr Ala Ser Trp Asn Val Pro
    610                 615
```

<210> 129
<211> 1854
<212> DNA
<213> Environmental

<400> 129

```
atgcgttgcc gccgtggcag ggacgggtgt tggtgcgggc ggcgtaatgc gctgccgcga      60
cacccgcgtg aacaaaataa tatgaattat ttgaatagga tgggggtgtc aagaatgaca     120
aaatctcgag agttgcggtg ttcatggaaa gtatttgttg ttgggtgcct gttgtggatg     180
gcttggggat cttccgcgtc cgccggcgta ttgatgcaag gcttctactg ggacgccagt     240
accgggacca gtgattcgtg gtggacgcat ttggccaagc aagccaacgg tctaaaacgg     300
gcggggttca ccgccgtatg gattcctccg gtgcttaaag gggcttcagg gggctattcc     360
aacgggtacg atccctttga cgactatgat atcggaagca aggaccagaa aggtaccgtg     420
gcgacgcgat gggggacgcg agaagaactg caacgtgccg tggccgtgat gcgcgcgaac     480
ggtctggatg tgtatgtgga tctggtgctg aaccaccgca acggggacga cgggaattgg     540
aattttcatt acaaagatgc gtacggcaaa gtgggttacg ggcggtttca aaaggggttt     600
tacgattttc accccaacta caacattcag gatgccaatg ttcccaacga ggattccagc     660
ttcgggcgcg atttagccca tgacaatccg tatgtggccg atggactgaa ggctgcaggc     720
gattggctga ccaaagccct cgatgttcag ggatatcgtc tggattacgt gaaaggcatc     780
agctacacct tcctgaaaag ttatctgtcc tatggggcca tgaacggaaa atttgccgtc     840
ggtgagtact gggatgccaa ccgggatacg ttgaactggt gggcgaacac ggcgatggaa     900
gggcgggccc atgtgtttga ttttgcgttg cgcgaggagc tgaaaaacat gtgcaatgcg     960
gacgggtact acgacatgcg tcgattggac cacgcgggtc tggtcggaat cgacccgtgg    1020
aaggcggtga cgtttgtcga aaaccatgat acggatcggc acgaccccat ctacaataac    1080
aagcatttgg cgtatgccta catcttgacg tcggaagggt atccgacggt gttctggaag    1140
gattactacc aatacggaat gaagccgatc atcgacaacc tcatttggat ccacgaacac    1200
attgcgtacg gaacgaccca agagcgttgg aaagacgaag atgtctttgt gtatgagcgg    1260
accggaggca agcggctatt ggtggggctt aacgacaatc gcgccaccag caaaacggtc    1320
accgtacaga ccggctttgg tgccaacgtg gccttgcacg actacaccgg caacggcccc    1380
gatctccgta ccgacgccta cggtcgggta accttgacca ttcctgcaaa cgggtacgtg    1440
gcctattccg ttccgggcat ctccggatcc tttgtgccgg tcgagaaaac cgtgacgcag    1500
gagtttgccg gggcgtccga cttggatatt cgtccggccg ataacacgca atttgtgcag    1560
gtcgggcgga tatacgccaa ggcaaacaag ccggttacag cggaattgta ttgggatgcc    1620
aaagactgga cgacctccac gtcgattctc ctagaagtgc gttcggcttc gggaacgctc    1680
atcacgacaa agaccgtgac ccaattgtcg tcccagggta cccgcgtttc cttcacgcct    1740
tcggctaccg gatggtacgt cttttccatt cgaagctata acacgccttc gacgaaccca    1800
aagccggcct actggttaaa ggtaacgtat acggcgccgc aattgcttca gtaa          1854
```

<210> 130
<211> 617
<212> PRT

<213> Environmental

<400> 130

```
Met Arg Cys Arg Arg Gly Arg Asp Gly Cys Trp Cys Gly Arg Arg Asn
 1               5                  10                  15
Ala Leu Pro Arg His Pro Arg Glu Gln Asn Asn Met Asn Tyr Leu Asn
            20                  25                  30
Arg Met Gly Val Ser Arg Met Thr Lys Ser Arg Glu Leu Arg Cys Ser
        35                  40                  45
Trp Lys Val Phe Val Val Gly Cys Leu Leu Trp Met Ala Trp Gly Ser
    50                  55                  60
Ser Ala Ser Ala Gly Val Leu Met Gln Gly Phe Tyr Trp Asp Ala Ser
65                  70                  75                  80
Thr Gly Thr Ser Asp Ser Trp Trp Thr His Leu Ala Lys Gln Ala Asn
                85                  90                  95
Gly Leu Lys Arg Ala Gly Phe Thr Ala Val Trp Ile Pro Pro Val Leu
            100                 105                 110
Lys Gly Ala Ser Gly Gly Tyr Ser Asn Gly Tyr Asp Pro Phe Asp Asp
        115                 120                 125
Tyr Asp Ile Gly Ser Lys Asp Gln Lys Gly Thr Val Ala Thr Arg Trp
    130                 135                 140
Gly Thr Arg Glu Glu Leu Gln Arg Ala Val Ala Val Met Arg Ala Asn
145                 150                 155                 160
Gly Leu Asp Val Tyr Val Asp Leu Val Leu Asn His Arg Asn Gly Asp
                165                 170                 175
Asp Gly Asn Trp Asn Phe His Tyr Lys Asp Ala Tyr Gly Lys Val Gly
            180                 185                 190
Tyr Gly Arg Phe Gln Lys Gly Phe Tyr Asp Phe His Pro Asn Tyr Asn
        195                 200                 205
Ile Gln Asp Ala Asn Val Pro Asn Glu Asp Ser Ser Phe Gly Arg Asp
    210                 215                 220
Leu Ala His Asp Asn Pro Tyr Val Ala Asp Gly Leu Lys Ala Ala Gly
225                 230                 235                 240
Asp Trp Leu Thr Lys Ala Leu Asp Val Gln Gly Tyr Arg Leu Asp Tyr
                245                 250                 255
Val Lys Gly Ile Ser Tyr Thr Phe Leu Lys Ser Tyr Leu Ser Tyr Gly
            260                 265                 270
Ala Met Asn Gly Lys Phe Ala Val Gly Glu Tyr Trp Asp Ala Asn Arg
        275                 280                 285
Asp Thr Leu Asn Trp Trp Ala Asn Thr Ala Met Glu Gly Arg Ala His
    290                 295                 300
Val Phe Asp Phe Ala Leu Arg Glu Glu Leu Lys Asn Met Cys Asn Ala
305                 310                 315                 320
Asp Gly Tyr Tyr Asp Met Arg Arg Leu Asp His Ala Gly Leu Val Gly
                325                 330                 335
Ile Asp Pro Trp Lys Ala Val Thr Phe Val Glu Asn His Asp Thr Asp
            340                 345                 350
Arg His Asp Pro Ile Tyr Asn Asn Lys His Leu Ala Tyr Ala Tyr Ile
        355                 360                 365
Leu Thr Ser Glu Gly Tyr Pro Thr Val Phe Trp Lys Asp Tyr Tyr Gln
    370                 375                 380
Tyr Gly Met Lys Pro Ile Ile Asp Asn Leu Ile Trp Ile His Glu His
385                 390                 395                 400
Ile Ala Tyr Gly Thr Thr Gln Glu Arg Trp Lys Asp Glu Asp Val Phe
                405                 410                 415
Val Tyr Glu Arg Thr Gly Gly Lys Arg Leu Leu Val Gly Leu Asn Asp
            420                 425                 430
```

```
Asn Arg Ala Thr Ser Lys Thr Val Thr Val Gln Thr Gly Phe Gly Ala
        435                 440                 445
Asn Val Ala Leu His Asp Tyr Thr Gly Asn Gly Pro Asp Leu Arg Thr
    450                 455                 460
Asp Ala Tyr Gly Arg Val Thr Leu Thr Ile Pro Ala Asn Gly Tyr Val
465                 470                 475                 480
Ala Tyr Ser Val Pro Gly Ile Ser Gly Ser Phe Val Pro Val Glu Lys
                485                 490                 495
Thr Val Thr Gln Glu Phe Ala Gly Ala Ser Asp Leu Asp Ile Arg Pro
            500                 505                 510
Ala Asp Asn Thr Gln Phe Val Gln Val Gly Arg Ile Tyr Ala Lys Ala
        515                 520                 525
Asn Lys Pro Val Thr Ala Glu Leu Tyr Trp Asp Ala Lys Asp Trp Thr
    530                 535                 540
Thr Ser Thr Ser Ile Leu Leu Glu Val Arg Ser Ala Ser Gly Thr Leu
545                 550                 555                 560
Ile Thr Thr Lys Thr Val Thr Gln Leu Ser Ser Gln Gly Thr Arg Val
                565                 570                 575
Ser Phe Thr Pro Ser Ala Thr Gly Trp Tyr Val Phe Ser Ile Arg Ser
            580                 585                 590
Tyr Asn Thr Pro Ser Thr Asn Pro Lys Pro Ala Tyr Trp Leu Lys Val
        595                 600                 605
Thr Tyr Thr Ala Pro Gln Leu Leu Gln
    610                 615
```

<210> 131
<211> 1881
<212> DNA
<213> Environmental

<400> 131

```
atgccgcagc tttacccatt gccgccgcgc tggcggcgcg cggcccggca gggcctggcc      60
gccttgacgc tggccaccac ggccctgggc atctcgacgg cccaggccca gagtgcaccg     120
cgcacggcct tcgtgcatct gttcgaatgg aagtggaccg acatcgcgcg cgagtgcgag     180
accttcctcg ggcccaaggg cttcgcggcg gtgcaggtgt cgcccccgaa cgagcacaac     240
tgggtgacca gcggtgatgg tgcaccttat ccgtggtgga tgcgctacca gccggtgagc     300
tacagcctgg accgcagccg cagcggcacg cgcgccgagt tccaggacat ggtcaaccga     360
tgcaatgccg tgggcgtggg catctacgtg gacgccgtga tcaatcacat gtccggcggc     420
acgggcggca cctcgagcgc tgggcgcagc tggagctatc acaactaccc tgggctctat     480
ggccccaacg acttccacca gccggtgtgc agcatcacca actacgggga tgcgaacaat     540
gtgcagcgtt gcgagctctc gggcttgcag gacctggaca ctgggagcgc ttatgtgcgc     600
ggcaagatcg ccgactatct ggtggatctg gtcaacatgg gggtcaaggg cttccgggtg     660
gatgcggcca agcacatcag cccgaccgac ctgggcgcca tcatcgatgc ggtcaacagc     720
cgcaccggcg cgaaccgccc tttctggttt ctggaggtga ttggcgcggc cggcgaggca     780
gtgcagccga accagtactt ctcgctcggc ggcggccagg tcaccgtgac cgagttcaac     840
tatgggaagc aaatcttcgg caagttcgcc ggtggcggcc gtctggccga gctgcgcagc     900
ttcggtgaaa cctggggcct gatgcccagc agcaaagcga ttgctttcat cgacaaccac     960
gacaagcagc gcggtcatgg cggcggtggc aactatctga cctaccacca tggctcgacc    1020
tacgatctgg ccaacatctt catgctggct tggccttatg gctacccggc gctgatgtcc    1080
agctatgcct tcaaccgcag cacggcctac gacacgagct ttggcccgcc acacgacagt    1140
ggtggcgcca cccgtggccc ctgggatggt ggcggcagcc agccggcctg cttcaaccag    1200
agcatcggtg gctgggtgtg tgagcaccgc tggcggggca tcgccaatat ggtggccttc    1260
cgcaacgcca cgctgcccaa ctggaccgtg accgactggt gggacaacgg caacaaccag    1320
atcgctttcg ggcggggtga caagggcttc gtggtgatca accgcgaaga cgccgcgctg    1380
acgcgcaact tcaagaccag cctgccagcc ggccagtact gcgatgtcat ctccggggac    1440
ttcaacaatg gtcagtgcac gggccatgtg gtgacggtcg atgccggcgg ctacgtgacg    1500
ctgacggccg ggcccaatgg tgcggcggcc atccacgtgg gcgcccgtct ggacggcgcc    1560
```

```
tctcagccgc cgacgaccgc ctcggtgacg ttcaacgcgt cggccgatac cttttgggga    1620
cagaacctgt tcgtcgtggg caaccacagc gcactgggca actggtcgcc ggcggccgcc    1680
aggccgatga cttggatttc cggttcgggc acgcgcggga actggcgcgc ggtgctcaat    1740
ttgccggcca ataccaccta ccaatacaag ttcatcaaga aggacggggc tggaaacgtg    1800
gtttgggagg gcggtggcaa tcgcgtcgtg accacgccgt ctgggggcgg atcggtgagc    1860
acgggcggca attggcagta g                                              1881
```

<210> 132
<211> 626
<212> PRT
<213> Environmental

<400> 132

```
Met Pro Gln Leu Tyr Pro Leu Pro Pro Arg Trp Arg Arg Ala Ala Arg
 1               5                  10                  15
Gln Gly Leu Ala Ala Leu Thr Leu Ala Thr Thr Ala Leu Gly Ile Ser
            20                  25                  30
Thr Ala Gln Ala Gln Ser Ala Pro Arg Thr Ala Phe Val His Leu Phe
        35                  40                  45
Glu Trp Lys Trp Thr Asp Ile Ala Arg Glu Cys Glu Thr Phe Leu Gly
    50                  55                  60
Pro Lys Gly Phe Ala Ala Val Gln Val Ser Pro Pro Asn Glu His Asn
65                  70                  75                  80
Trp Val Thr Ser Gly Asp Gly Ala Pro Tyr Pro Trp Trp Met Arg Tyr
                85                  90                  95
Gln Pro Val Ser Tyr Ser Leu Asp Arg Ser Arg Ser Gly Thr Arg Ala
            100                 105                 110
Glu Phe Gln Asp Met Val Asn Arg Cys Asn Ala Val Gly Val Gly Ile
        115                 120                 125
Tyr Val Asp Ala Val Ile Asn His Met Ser Gly Gly Thr Gly Gly Thr
    130                 135                 140
Ser Ser Ala Gly Arg Ser Trp Ser Tyr His Asn Tyr Pro Gly Leu Tyr
145                 150                 155                 160
Gly Pro Asn Asp Phe His Gln Pro Val Cys Ser Ile Thr Asn Tyr Gly
                165                 170                 175
Asp Ala Asn Asn Val Gln Arg Cys Glu Leu Ser Gly Leu Gln Asp Leu
            180                 185                 190
Asp Thr Gly Ser Ala Tyr Val Arg Gly Lys Ile Ala Asp Tyr Leu Val
        195                 200                 205
Asp Leu Val Asn Met Gly Val Lys Gly Phe Arg Val Asp Ala Ala Lys
    210                 215                 220
His Ile Ser Pro Thr Asp Leu Gly Ala Ile Ile Asp Ala Val Asn Ser
225                 230                 235                 240
Arg Thr Gly Ala Asn Arg Pro Phe Trp Phe Leu Glu Val Ile Gly Ala
                245                 250                 255
Ala Gly Glu Ala Val Gln Pro Asn Gln Tyr Phe Ser Leu Gly Gly Gly
            260                 265                 270
Gln Val Thr Val Thr Glu Phe Asn Tyr Gly Lys Gln Ile Phe Gly Lys
        275                 280                 285
Phe Ala Gly Gly Gly Arg Leu Ala Glu Leu Arg Ser Phe Gly Glu Thr
    290                 295                 300
Trp Gly Leu Met Pro Ser Ser Lys Ala Ile Ala Phe Ile Asp Asn His
305                 310                 315                 320
Asp Lys Gln Arg Gly His Gly Gly Gly Gly Asn Tyr Leu Thr Tyr His
                325                 330                 335
His Gly Ser Thr Tyr Asp Leu Ala Asn Ile Phe Met Leu Ala Trp Pro
            340                 345                 350
```

```
Tyr Gly Tyr Pro Ala Leu Met Ser Ser Tyr Ala Phe Asn Arg Ser Thr
        355                 360                 365
Ala Tyr Asp Thr Ser Phe Gly Pro Pro His Asp Ser Gly Gly Ala Thr
    370                 375                 380
Arg Gly Pro Trp Asp Gly Gly Gly Ser Gln Pro Ala Cys Phe Asn Gln
385                 390                 395                 400
Ser Ile Gly Gly Trp Val Cys Glu His Arg Trp Arg Gly Ile Ala Asn
                405                 410                 415
Met Val Ala Phe Arg Asn Ala Thr Leu Pro Asn Trp Thr Val Thr Asp
            420                 425                 430
Trp Trp Asp Asn Gly Asn Asn Gln Ile Ala Phe Gly Arg Gly Asp Lys
        435                 440                 445
Gly Phe Val Val Ile Asn Arg Glu Asp Ala Ala Leu Thr Arg Asn Phe
    450                 455                 460
Lys Thr Ser Leu Pro Ala Gly Gln Tyr Cys Asp Val Ile Ser Gly Asp
465                 470                 475                 480
Phe Asn Asn Gly Gln Cys Thr Gly His Val Val Thr Val Asp Ala Gly
                485                 490                 495
Gly Tyr Val Thr Leu Thr Ala Gly Pro Asn Gly Ala Ala Ala Ile His
            500                 505                 510
Val Gly Ala Arg Leu Asp Gly Ala Ser Gln Pro Pro Thr Thr Ala Ser
        515                 520                 525
Val Thr Phe Asn Ala Ser Ala Asp Thr Phe Trp Gly Gln Asn Leu Phe
    530                 535                 540
Val Val Gly Asn His Ser Ala Leu Gly Asn Trp Ser Pro Ala Ala Ala
545                 550                 555                 560
Arg Pro Met Thr Trp Ile Ser Gly Ser Gly Thr Arg Gly Asn Trp Arg
                565                 570                 575
Ala Val Leu Asn Leu Pro Ala Asn Thr Thr Tyr Gln Tyr Lys Phe Ile
            580                 585                 590
Lys Lys Asp Gly Ala Gly Asn Val Val Trp Glu Gly Gly Gly Asn Arg
        595                 600                 605
Val Val Thr Thr Pro Ser Gly Gly Gly Ser Val Ser Thr Gly Gly Asn
    610                 615                 620
Trp Gln
625
```

<210> 133
<211> 1638
<212> DNA
<213> Environmental

<400> 133

```
atgaataatg tgaaaaaagt atggttgtat tattctataa ttgctacctt agttatttcc      60
tttttcacac ctttttcaac agcacaagct aatactgcac ctgtcaacgg aacaatgatg     120
caatatttcg aatgggattt accgaatgat gggacgcttt ggacgaaagt aaaaaatgaa     180
gctaccaatc tttcttcgct aggtattaca gcgttatggc tccctccagc atataaagga     240
acgagccaaa gcgatgtcgg atatggcgtg tacgatttat atgaccttgg ggaatttaat     300
caaaaaggga cgatccgaac gaaatacgga acaaaagcac aatatattca agccatccaa     360
gctgccaaag ccgcagggat gcaagtatat gcagatgttg tatttaatca taaggcgggg     420
gctgacggca cagaatttgt cgatgcagtt gaggtaaacc cttctaatcg aaatcaagaa     480
acatctggca catatcaaat tcaagcatgg acaaaatttg attttcctgg tcgtggaaac     540
acatactcca gcttcaaatg gcgctggtat cattttgacg gtaccgattg ggatgaaagt     600
cgtaaattaa atcgtattta caaattccgc ggtacaggaa aagcgtggga ctgggaagtc     660
gatacagaaa acggaaacta tgattattta atgttcgctg atttagatat ggatcaccct     720
gaagttgtga cagagttaaa aaactgggga aaatggtatg taaatacgac aaatgtagac     780
ggatttcgtt tggatgccgt aaaacatatt aaatacagct ttttccctga ctggctaaca     840
```

```
tatgtacgta atcaaacagg aaaaaattta tttgctgttg gggaattttg gagctatgac     900
gtcaataagc tgcataacta cattacaaaa acaaatggat cgatgtcgtt atttgatgca     960
cctttgcata acaactttta tatcgcttcc aaatcgagtg gatattttga catgcgttat    1020
ttattgaata atacattaat gaaagatcaa ccttcactcg ctgtaacact tgtcgataac    1080
catgatacac aaccaggtca atctttacaa tcatgggtag aagcttggtt taaaccgctt    1140
gcttacgcct ttatttttaac aagacaagag gggtatcctt gcgtatttta cggtgactat    1200
tacggaatcc cgaaatacaa tattccggga ttaaaaagta aaattgatcc gcttttaatt    1260
gctcgtcgtg attatgctta tggaacacaa cgtgattaca ttgatcatca agacattatc    1320
ggatggacac gagaaggcat tgatgcaaaa ccgaactctg gacttgcggc tttaattacc    1380
gacggccctg gcggaagtaa atggatgtat gtcggtaaaa aacatgctgg gaaagtgttt    1440
tatgatttaa ctggaaatcg aagtgacaca gtaacgatta atgcggacgg ttggggagaa    1500
tttaaagtaa acggcggctc cgtttcgatt tgggtggcta aaacatcaaa cgtcacattt    1560
acagtcaata acgccacaac aacaagtgga caaaacgtat atgttgttgg caacattcca    1620
gagctaggca attctttg                                                 1638
```

<210> 134
<211> 546
<212> PRT
<213> Environmental

<400> 134

```
Met Asn Asn Val Lys Lys Val Trp Leu Tyr Tyr Ser Ile Ile Ala Thr
 1               5                  10                  15
Leu Val Ile Ser Phe Phe Thr Pro Phe Ser Thr Ala Gln Ala Asn Thr
            20                  25                  30
Ala Pro Val Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Asp Leu Pro
        35                  40                  45
Asn Asp Gly Thr Leu Trp Thr Lys Val Lys Asn Glu Ala Thr Asn Leu
    50                  55                  60
Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys Gly
65                  70                  75                  80
Thr Ser Gln Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp Leu
                85                  90                  95
Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly Thr Lys
            100                 105                 110
Ala Gln Tyr Ile Gln Ala Ile Gln Ala Ala Lys Ala Ala Gly Met Gln
        115                 120                 125
Val Tyr Ala Asp Val Val Phe Asn His Lys Ala Gly Ala Asp Gly Thr
    130                 135                 140
Glu Phe Val Asp Ala Val Glu Val Asn Pro Ser Asn Arg Asn Gln Glu
145                 150                 155                 160
Thr Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe Pro
                165                 170                 175
Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His Phe
            180                 185                 190
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
        195                 200                 205
Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu Asn
    210                 215                 220
Gly Asn Tyr Asp Tyr Leu Met Phe Ala Asp Leu Asp Met Asp His Pro
225                 230                 235                 240
Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn Thr
                245                 250                 255
Thr Asn Val Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Tyr
            260                 265                 270
Ser Phe Phe Pro Asp Trp Leu Thr Tyr Val Arg Asn Gln Thr Gly Lys
        275                 280                 285
```

```
Asn Leu Phe Ala Val Gly Glu Phe Trp Ser Tyr Asp Val Asn Lys Leu
    290                 295                 300
His Asn Tyr Ile Thr Lys Thr Asn Gly Ser Met Ser Leu Phe Asp Ala
305                 310                 315                 320
Pro Leu His Asn Asn Phe Tyr Ile Ala Ser Lys Ser Ser Gly Tyr Phe
                325                 330                 335
Asp Met Arg Tyr Leu Leu Asn Asn Thr Leu Met Lys Asp Gln Pro Ser
            340                 345                 350
Leu Ala Val Thr Leu Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser
        355                 360                 365
Leu Gln Ser Trp Val Glu Ala Trp Phe Lys Pro Leu Ala Tyr Ala Phe
    370                 375                 380
Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp Tyr
385                 390                 395                 400
Tyr Gly Ile Pro Lys Tyr Asn Ile Pro Gly Leu Lys Ser Lys Ile Asp
                405                 410                 415
Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln Arg Asp
            420                 425                 430
Tyr Ile Asp His Gln Asp Ile Ile Gly Trp Thr Arg Glu Gly Ile Asp
        435                 440                 445
Ala Lys Pro Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly
    450                 455                 460
Gly Ser Lys Trp Met Tyr Val Gly Lys Lys His Ala Gly Lys Val Phe
465                 470                 475                 480
Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ala Asp
                485                 490                 495
Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Ile Trp Val
            500                 505                 510
Ala Lys Thr Ser Asn Val Thr Phe Thr Val Asn Asn Ala Thr Thr Thr
        515                 520                 525
Ser Gly Gln Asn Val Tyr Val Val Gly Asn Ile Pro Glu Leu Gly Asn
    530                 535                 540
Ser Leu
545
```

<210> 135
<211> 1935
<212> DNA
<213> Environmental

<400> 135

```
gtgacaggca ccccgtcttt atacattcct ccacataaaa taaccataca gctttcaaat      60
ttgttgaaat gtataaaaat aaaaaatagt attgtaagcg ttaacatccg tcattataat     120
aacttcaaac gcgtttatgt tttaatgcaa acgtttgcat cctcatttta tttaaagaaa     180
ggatgtgtgt gcatgaatta tttgaaaaaa gtgtggttgt attacgctat cgtcgctacc     240
ttaatcattt cctttcttac gccctttttca actgcacaag ccaacactgc accagtcaac     300
ggaacgatga tgcaatattt cgaatgggat ttaccgaatg atggcacact ttggacgaaa     360
gtaaaaaacg aagcaagcag cctttcttct ttaggtatta ctgcgttatg gttaccacct     420
gcatacaaag gaacgagcca aggggatgtc gggtatggcg tgtacgattt gtatgactta     480
ggagaattta atcaaaaagg gacgattcga acgaaatacg gaacaaaaac gcaatattta     540
caagccattc aagcggcaaa aagcgctggc atgcaagtat acgctgatgt cgtatttaat     600
cacaaggcgg gggcagatag tacagaatgg gttgacgcag tcgaagtgaa tccttctaat     660
cgaaaccaag aaacatctgg cacatatcaa attcaagcat ggacaaaatt tgatttccct     720
gaccgtggga acacatactc aagctttaaa tggcgctggt atcattttga cggtacggat     780
tgggatgaaa gtcgaaaact aaatcgcatt tacaaatttc gtggcacagg aaaagcatgg     840
gattgggaag tagacacaga gaacggaaac tatgactact taatgtttgc tgatttagat     900
atggatcacc ctgaagtcgt gacagagcta aaaaactggg gaacatggta cgtcaatacg     960
```

```
acaaatgtcg atgggtttcg cttagatgca gtaaagcata ttaaatatag ctttttccca    1020
gattggttaa catatgtgcg ctcacaaaca caaaaaaatc tgtttgcagt aggagaattt    1080
tggagctacg atgtcaataa actgcataac tacattacaa aaacaagtgg aaccatgtcg    1140
ttatttgatg cgccacttca taacaacttt tacactgctt caaaatctag cgggtatttt    1200
gacatgcgct atttgttaaa taatacgttg atgaaagacc agccttctct tgcggtcaca    1260
ctcgttgata atcatgacac gcaaccggga caatctttac aatcatgggt agagccttgg    1320
tttaagccgc ttgcttatgc ctttattttg acaagacaag aaggatatcc ttgcgtattt    1380
tacggcgact attacggcat ccctaaatac aatattccgg gattgaaaag taaaatcgat    1440
ccgcttctca ttgcccgtag agactacgca tacggaacac aacgtgatta tattgaccat    1500
caagacatta ttggatggac acgggaagga attgactcaa aaccgaactc tggacttgcg    1560
gctttaatta ctgacggtcc tggtggaagt aaatggatgt atgtaggtaa aaagcatgct    1620
ggaaaagtgt tttacgatct cactggaaat cgaagcgata cggtaacgat taatgcagac    1680
ggctggggag agtttaaagt aaacggtggc tccgtttcca tttgggttgc caaaacatca    1740
caagtcacgt ttaccgtcaa caatgcgaca acgacaagcg gacaaaatgt gtatgtcgtt    1800
ggcaacattc cagagctcgg aaattggaac acagcaaacg caatcaaaat gaccccatct    1860
tcttatccaa cgtggaaaac aaccattgct cttccacaag gaaaagcaat tggcggcgta    1920
cgccatggcc cttga                                                     1935

<210> 136
<211> 644
<212> PRT
<213> Environmental

<400> 136
Val Thr Gly Thr Pro Ser Leu Tyr Ile Pro Pro His Lys Ile Thr Ile
 1               5                  10                  15
Gln Leu Ser Asn Leu Leu Lys Cys Ile Lys Ile Lys Asn Ser Ile Val
            20                  25                  30
Ser Val Asn Ile Arg His Tyr Asn Asn Phe Lys Arg Val Tyr Val Leu
        35                  40                  45
Met Gln Thr Phe Ala Ser Ser Phe Tyr Leu Lys Lys Gly Cys Val Cys
    50                  55                  60
Met Asn Tyr Leu Lys Lys Val Trp Leu Tyr Tyr Ala Ile Val Ala Thr
65                  70                  75                  80
Leu Ile Ile Ser Phe Leu Thr Pro Phe Ser Thr Ala Gln Ala Asn Thr
                85                  90                  95
Ala Pro Val Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Asp Leu Pro
            100                 105                 110
Asn Asp Gly Thr Leu Trp Thr Lys Val Lys Asn Glu Ala Ser Ser Leu
        115                 120                 125
Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys Gly
    130                 135                 140
Thr Ser Gln Gly Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp Leu
145                 150                 155                 160
Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly Thr Lys
                165                 170                 175
Thr Gln Tyr Leu Gln Ala Ile Gln Ala Ala Lys Ser Ala Gly Met Gln
            180                 185                 190
Val Tyr Ala Asp Val Val Phe Asn His Lys Ala Gly Ala Asp Ser Thr
        195                 200                 205
Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asn Arg Asn Gln Glu
    210                 215                 220
Thr Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe Pro
225                 230                 235                 240
Asp Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His Phe
                245                 250                 255
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
```

```
            260                 265                 270
Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu Asn
        275                 280                 285
Gly Asn Tyr Asp Tyr Leu Met Phe Ala Asp Leu Asp Met Asp His Pro
    290                 295                 300
Glu Val Val Thr Glu Leu Lys Asn Trp Gly Thr Trp Tyr Val Asn Thr
305                 310                 315                 320
Thr Asn Val Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Tyr
                325                 330                 335
Ser Phe Phe Pro Asp Trp Leu Thr Tyr Val Arg Ser Gln Thr Gln Lys
            340                 345                 350
Asn Leu Phe Ala Val Gly Glu Phe Trp Ser Tyr Asp Val Asn Lys Leu
        355                 360                 365
His Asn Tyr Ile Thr Lys Thr Ser Gly Thr Met Ser Leu Phe Asp Ala
    370                 375                 380
Pro Leu His Asn Asn Phe Tyr Thr Ala Ser Lys Ser Ser Gly Tyr Phe
385                 390                 395                 400
Asp Met Arg Tyr Leu Leu Asn Asn Thr Leu Met Lys Asp Gln Pro Ser
                405                 410                 415
Leu Ala Val Thr Leu Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser
            420                 425                 430
Leu Gln Ser Trp Val Glu Pro Trp Phe Lys Pro Leu Ala Tyr Ala Phe
        435                 440                 445
Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp Tyr
    450                 455                 460
Tyr Gly Ile Pro Lys Tyr Asn Ile Pro Gly Leu Lys Ser Lys Ile Asp
465                 470                 475                 480
Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln Arg Asp
                485                 490                 495
Tyr Ile Asp His Gln Asp Ile Ile Gly Trp Thr Arg Glu Gly Ile Asp
            500                 505                 510
Ser Lys Pro Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly
        515                 520                 525
Gly Ser Lys Trp Met Tyr Val Gly Lys Lys His Ala Gly Lys Val Phe
    530                 535                 540
Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ala Asp
545                 550                 555                 560
Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Ile Trp Val
                565                 570                 575
Ala Lys Thr Ser Gln Val Thr Phe Thr Val Asn Asn Ala Thr Thr Thr
            580                 585                 590
Ser Gly Gln Asn Val Tyr Val Val Gly Asn Ile Pro Glu Leu Gly Asn
        595                 600                 605
Trp Asn Thr Ala Asn Ala Ile Lys Met Thr Pro Ser Ser Tyr Pro Thr
    610                 615                 620
Trp Lys Thr Thr Ile Ala Leu Pro Gln Gly Lys Ala Ile Gly Gly Val
625                 630                 635                 640
Arg His Gly Pro
```

<210> 137
<211> 1320
<212> DNA
<213> Environmental

<400> 137
gtgggacggg caggcttggc gcatcactcg aacacttccg ccaaggggac atacgggtca 60

```
cctctcgaac tgcgtccgga tcgccccgcc gtggccgggg cggtcgagct tgaagatgtc     120
cagcggggag ccgccgccga ggatcacccc ggcggcgtac tcgcccaggg cggggctcag     180
cttgaagccg tggccggagc cgcctcccag gagccagacg ttggaggccc gcggatggcg     240
gtcgaggagg aggtggccgt cggggctgtt ctcgtactgg cagacgcggg tctcgaccag     300
cggcgcgtcc ttcagggccg ggaaccggcg ggccacctcg gcccgggccg cttccagcag     360
ggccggggtg atcgtccgct cgcccgccgt gggatcgatg ggctcgcccc gggtgtcgtc     420
cgccaccttg aagccgcggt gctcgttgcc ggggatgccg tagtagatcc gctcgccgag     480
atcgacccag accggacagc cgccctcctg gaagcgcggg tcgcccggcg gcgtgccgaa     540
gaagaacacc tcctggcggg tgttgcggag gaaccgctca ccgatcacgt ccgggaacag     600
cccggccagc cagggaccgc aggcgaagac gtagaggtcg gccgcgagag tggagccgtc     660
cgaaaggtga agccgctcca agggccccgg gaccatggcg gcctgccggt actccccgcc     720
ctcgccctgg aacagctcca ccacggtccg gcaggcgcgc cgggcgaaca gggcgccggc     780
ttcctcctcg taccagatcg tgcggacgcc gtcgaaatcg acctgggggа agcggctccg     840
ggcctccccc tgagacagct cggcgaccgg cagccccgcg tcctccagaa aaggaaggga     900
gtcgcggacg tagctgtcgt cctcgccgca catccagagg accccggtcc ttttgtacag     960
ccggtaaccg gactggactt cggcgtcccg ccagagctcg aaggagcggg cgacccactc    1020
cacgtacaga cggtcgggtc cgtaggcgcc gcggatgatc cgcgtctcgc caccggagct    1080
ggagcgggag tgccccggac cccaggcgtc caggagggtc acccgggctc cgcggcggag    1140
gagatgcagg gcggtccagc cgccgaaggc gccggcgccg acgacggcga tatggggatg    1200
ggagggcatg gcgggcgtaa ggttatcgca gcccgatcct tcgctggcat cccatctccg    1260
accggagtat cctggaaaat tcgaagaagg agatcgacat gcaatcgaac ggaaacgtga    1320
```

<210> 138
<211> 439
<212> PRT
<213> Environmental

<400> 138

```
Val Gly Arg Ala Gly Leu Ala His His Ser Asn Thr Ser Ala Lys Gly
 1               5                  10                  15
Thr Tyr Gly Ser Pro Leu Glu Leu Arg Pro Asp Arg Pro Ala Val Ala
            20                  25                  30
Gly Ala Val Glu Leu Glu Asp Val Gln Arg Gly Ala Ala Ala Glu Asp
        35                  40                  45
His Pro Gly Gly Val Leu Ala Gln Gly Gly Ala Gln Leu Glu Ala Val
    50                  55                  60
Ala Gly Ala Ala Ser Gln Glu Pro Asp Val Gly Gly Pro Arg Met Ala
65                  70                  75                  80
Val Glu Glu Glu Val Ala Val Gly Ala Val Leu Val Leu Ala Asp Ala
                85                  90                  95
Gly Leu Asp Gln Arg Arg Val Leu Gln Gly Arg Glu Pro Ala Gly His
            100                 105                 110
Leu Gly Pro Gly Arg Phe Gln Gln Gly Arg Gly Asp Arg Pro Leu Ala
        115                 120                 125
Arg Arg Gly Ile Asp Gly Leu Ala Pro Gly Val Val Arg His Leu Glu
    130                 135                 140
Ala Ala Val Leu Val Ala Gly Asp Ala Val Val Asp Pro Leu Ala Glu
145                 150                 155                 160
Ile Asp Pro Asp Arg Thr Ala Ala Leu Leu Glu Ala Arg Val Ala Arg
                165                 170                 175
Arg Arg Ala Glu Glu Glu His Leu Leu Ala Gly Val Ala Glu Glu Pro
            180                 185                 190
Leu Thr Asp His Val Arg Glu Gln Pro Gly Gln Pro Gly Thr Ala Gly
        195                 200                 205
Glu Asp Val Glu Val Gly Arg Glu Ser Gly Ala Val Arg Lys Val Lys
    210                 215                 220
Pro Leu Gln Gly Pro Arg Asp His Gly Gly Leu Pro Val Leu Pro Ala
```

```
225                 230                 235                 240
Leu Ala Leu Glu Gln Leu His His Gly Pro Ala Gly Ala Pro Gly Glu
                245                 250                 255
Gln Gly Ala Gly Phe Leu Leu Val Pro Asp Arg Ala Asp Ala Val Glu
            260                 265                 270
Ile Asp Leu Gly Glu Ala Ala Pro Gly Leu Pro Leu Arg Gln Leu Gly
        275                 280                 285
Asp Arg Gln Pro Arg Val Leu Gln Lys Arg Lys Gly Val Ala Asp Val
    290                 295                 300
Ala Val Val Leu Ala Ala His Pro Glu Asp Pro Gly Pro Phe Val Gln
305                 310                 315                 320
Pro Val Thr Gly Leu Asp Phe Gly Val Pro Pro Glu Leu Glu Gly Ala
                325                 330                 335
Gly Asp Pro Leu His Val Gln Thr Val Gly Ser Val Gly Ala Ala Asp
            340                 345                 350
Asp Pro Arg Leu Ala Thr Gly Ala Gly Ala Gly Val Pro Arg Thr Pro
        355                 360                 365
Gly Val Gln Glu Gly His Pro Gly Ser Ala Ala Glu Glu Met Gln Gly
    370                 375                 380
Gly Pro Ala Ala Glu Gly Ala Gly Ala Asp Asp Gly Asp Met Gly Met
385                 390                 395                 400
Gly Gly His Gly Gly Arg Lys Val Ile Ala Ala Arg Ser Phe Ala Gly
                405                 410                 415
Ile Pro Ser Pro Thr Gly Val Ser Trp Lys Ile Arg Arg Arg Arg Ser
            420                 425                 430
Thr Cys Asn Arg Thr Glu Thr
        435
```

<210> 139
<211> 1524
<212> DNA
<213> Environmental

<400> 139

```
atgaaaacat tcaaccttaa acccacactt ttacctttaa ctttgctgct gagttcgccg      60
gtattggcgg cacaaaatgg aactatgatg cagtatttcc attggtatgt gccaaatgac     120
ggcgcactct ggacacaagt tgaaaacaat gcgccagcac tatccgacaa cggttttaca     180
gcgctgtggt tgccaccagc atataaaggc gcaggtggta gcaacgacgt tggttacggt     240
gtttacgata tgtatgactt aggggagttt gatcaaaaag gatcggtacg aactaagtac     300
ggcaccaaag accaatatct aaatgccatc aaagcagcac acaaaaacaa tatccaaatt     360
tatggtgacg tagtgttcaa ccatcgtggc ggtgcagatg gcaagtcgtg ggtcgatacc     420
aagcgtgtgg attggaataa ccgcaatatt gaacttggcg ataaatggat tgaagcatgg     480
gttgaattta gcttcccagg acgtaacgat aaatactcag acttccattg gacgtggtat     540
cactttgatg gcgtcgattg ggatgacgca ggtaaagaga aagcgatctt taaattcaaa     600
ggtgatggta aagcatggga ttgggaagtc agttctgaaa aaggcaacta tgactacctc     660
atgtacgcag acttagacat ggatcaccca gaagtgaagc aagagctgaa agattggggt     720
gaatggtact taaacatgac gggtgttgat ggcttccgaa tggatgcagt gaaacacatc     780
aaatatcagt acctacaaga gtggatcgat tacttgcgta agaaaacggg caaagagctc     840
tttaccgttg gtgagtactg gaactacgac gtgaacaatc tgcacaactt tatgactaag     900
acttctggca gcatgtcatt gtttgatgcg cctttacata tgaacttcta taacgcttca     960
cgctctggtg gcaactttga tatgcgccga atcatggatg gcaccttgat gaaagacaac    1020
ccagtgaaag cagtaacact ggttgagaac catgatacgc aaccactaca ggccttagag    1080
tctccggtgg attggtggtt caaaccactt gcgtacgcgt tcattttgct tcgtgaggaa    1140
ggttatccgt cagtcttcta cgcagattac tacggtgcgc aatacagcga taaagggcac    1200
gatatcaaca tggtgaaagt gccttacatt gagcaattgg tgaaagcgcg taaagattat    1260
gcttatggta aacaacattc ttaccttgac cactgggatg tgattggttg gacacgagaa    1320
ggggatgcgg aacatccgaa ctctatggcg gttatcatga gtgatggtcc tggcggaaca    1380
```

```
aagtggatgt acacaggttc accgagcaca cgttatgtcg ataaactagg tattcgtacc    1440
gaagaagtat ggactaacgc tagtggatgg gccgaattcc cagtgaacgg cggatcggtt    1500
tctgtttggg ttggcgttaa ataa                                          1524

<210> 140
<211> 507
<212> PRT
<213> Environmental

<400> 140
Met Lys Thr Phe Asn Leu Lys Pro Thr Leu Leu Pro Leu Thr Leu Leu
 1               5                  10                  15
Leu Ser Ser Pro Val Leu Ala Ala Gln Asn Gly Thr Met Met Gln Tyr
            20                  25                  30
Phe His Trp Tyr Val Pro Asn Asp Gly Ala Leu Trp Thr Gln Val Glu
        35                  40                  45
Asn Asn Ala Pro Ala Leu Ser Asp Asn Gly Phe Thr Ala Leu Trp Leu
    50                  55                  60
Pro Pro Ala Tyr Lys Gly Ala Gly Gly Ser Asn Asp Val Gly Tyr Gly
65                  70                  75                  80
Val Tyr Asp Met Tyr Asp Leu Gly Glu Phe Asp Gln Lys Gly Ser Val
                85                  90                  95
Arg Thr Lys Tyr Gly Thr Lys Asp Gln Tyr Leu Asn Ala Ile Lys Ala
            100                 105                 110
Ala His Lys Asn Asn Ile Gln Ile Tyr Gly Asp Val Val Phe Asn His
        115                 120                 125
Arg Gly Gly Ala Asp Gly Lys Ser Trp Val Asp Thr Lys Arg Val Asp
    130                 135                 140
Trp Asn Asn Arg Asn Ile Glu Leu Gly Asp Lys Trp Ile Glu Ala Trp
145                 150                 155                 160
Val Glu Phe Ser Phe Pro Gly Arg Asn Asp Lys Tyr Ser Asp Phe His
                165                 170                 175
Trp Thr Trp Tyr His Phe Asp Gly Val Asp Trp Asp Asp Ala Gly Lys
            180                 185                 190
Glu Lys Ala Ile Phe Lys Phe Lys Gly Asp Gly Lys Ala Trp Asp Trp
        195                 200                 205
Glu Val Ser Ser Glu Lys Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp
    210                 215                 220
Leu Asp Met Asp His Pro Glu Val Lys Gln Glu Leu Lys Asp Trp Gly
225                 230                 235                 240
Glu Trp Tyr Leu Asn Met Thr Gly Val Asp Gly Phe Arg Met Asp Ala
                245                 250                 255
Val Lys His Ile Lys Tyr Gln Tyr Leu Gln Glu Trp Ile Asp Tyr Leu
            260                 265                 270
Arg Lys Lys Thr Gly Lys Glu Leu Phe Thr Val Gly Glu Tyr Trp Asn
        275                 280                 285
Tyr Asp Val Asn Asn Leu His Asn Phe Met Thr Lys Thr Ser Gly Ser
    290                 295                 300
Met Ser Leu Phe Asp Ala Pro Leu His Met Asn Phe Tyr Asn Ala Ser
305                 310                 315                 320
Arg Ser Gly Gly Asn Phe Asp Met Arg Arg Ile Met Asp Gly Thr Leu
                325                 330                 335
Met Lys Asp Asn Pro Val Lys Ala Val Thr Leu Val Glu Asn His Asp
            340                 345                 350
Thr Gln Pro Leu Gln Ala Leu Glu Ser Pro Val Asp Trp Trp Phe Lys
        355                 360                 365
Pro Leu Ala Tyr Ala Phe Ile Leu Leu Arg Glu Glu Gly Tyr Pro Ser
```

```
    370                 375                 380
Val Phe Tyr Ala Asp Tyr Tyr Gly Ala Gln Tyr Ser Asp Lys Gly His
385                 390                 395                 400
Asp Ile Asn Met Val Lys Val Pro Tyr Ile Glu Gln Leu Val Lys Ala
                405                 410                 415
Arg Lys Asp Tyr Ala Tyr Gly Lys Gln His Ser Tyr Leu Asp His Trp
            420                 425                 430
Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Ala Glu His Pro Asn Ser
        435                 440                 445
Met Ala Val Ile Met Ser Asp Gly Pro Gly Gly Thr Lys Trp Met Tyr
    450                 455                 460
Thr Gly Ser Pro Ser Thr Arg Tyr Val Asp Lys Leu Gly Ile Arg Thr
465                 470                 475                 480
Glu Glu Val Trp Thr Asn Ala Ser Gly Trp Ala Glu Phe Pro Val Asn
                485                 490                 495
Gly Gly Ser Val Ser Val Trp Val Gly Val Lys
            500                 505
```

<210> 141
<211> 1401
<212> DNA
<213> Environmental

<400> 141

```
atgaaaccaa taaataccct actcatatcc gcccttgctg tttgttcttt cagttccgcg      60
acttacgccg atactatttt gcacgcgttc aattggaagt attcagatgt gacggccaac     120
gcgaatcaaa ttgctcaagc tggttataag aaagtgcttg ttgcgcctgc aatgaaatcg     180
agtggcagcc aatggtgggc tcgctatcaa cctcaagatc tacgcactat cgattctcct     240
ttgggcaata aacaagattt agccgcaatg attgccgcac tcaaaggtgt gggcgtcgat     300
gtgtatgccg atgtggtact caaccatatg gcgaatgaaa gctggaagcg aagtgacttg     360
aattaccctg gcacagaagt gctaaacgat tatgctagcc gttcaagcta ctatgctgac     420
cagactctgt ttggcaacct agcacaaggt tatgtgtcag cgaacgactt tcatccagcg     480
ggctgtattt cagattggaa cgaccctggt catgttcagt attggcgttt gtgtggcgca     540
gatggtgatg taggtttacc tgaccttgat ccaaacaact gggtggtttc acaacagcgt     600
ttgtatctga aagcgctaaa agatatgggc atcaaagggt tccgaattga tgcagtgaag     660
cacatgagcc aataccaaat cgatcaggta ttcacgtctg aaattactgc gaacatgcat     720
gtgtttggtg aagtgattac tagcggtgga gcagggaata gcggctatga atcgttctta     780
gcgccttacc tgaataatac taatcactct gcctacgatt tcccgctgtt tgcatcgatt     840
cgctcggcat tttctatggg gggcggttta aatcaactgc atgatcctaa agcgtacggt     900
caggcacttg atgataatcg ctcgatcacc tttgcgatca cacatgatat tccaaccaat     960
gacggcttcc gctaccaaat tatggaccca caagacgagc agcttgctta cgcgtatatc    1020
cttggtaaag acggtggcac gccgctgatc tacagtgatg atcttcctga ttctgaagac    1080
aaggataacg gtcgttgggg caatgtttgg aacagttcga caatgaaaaa catgttgagc    1140
ttccataacg cgatgcaagg caaaacaatg acgatgattt ctagcgacca ttgcactttg    1200
ttgtttaagc gtggcaaaga aggtgttgtg ggtattaaca agtgtggtga aacgcgtggc    1260
gtgacggttg atacctacca acatgagttt aattggcatg ttcaatacaa agacgtgtta    1320
agcagcgcaa cagaaaccgt gacttctcgt taccatacgt tcaatctacc accacgcagt    1380
gcgcgtatgt ttaagctgta g                                              1401
```

<210> 142
<211> 466
<212> PRT
<213> Environmental

<400> 142

```
Met Lys Pro Ile Asn Thr Leu Leu Ile Ser Ala Leu Ala Val Cys Ser
 1               5                  10                  15
```

```
Phe Ser Ser Ala Thr Tyr Ala Asp Thr Ile Leu His Ala Phe Asn Trp
            20                  25                  30
Lys Tyr Ser Asp Val Thr Ala Asn Ala Asn Gln Ile Ala Gln Ala Gly
        35                  40                  45
Tyr Lys Lys Val Leu Val Ala Pro Ala Met Lys Ser Ser Gly Ser Gln
    50                  55                  60
Trp Trp Ala Arg Tyr Gln Pro Gln Asp Leu Arg Thr Ile Asp Ser Pro
65                  70                  75                  80
Leu Gly Asn Lys Gln Asp Leu Ala Ala Met Ile Ala Ala Leu Lys Gly
                85                  90                  95
Val Gly Val Asp Val Tyr Ala Asp Val Val Leu Asn His Met Ala Asn
            100                 105                 110
Glu Ser Trp Lys Arg Ser Asp Leu Asn Tyr Pro Gly Thr Glu Val Leu
        115                 120                 125
Asn Asp Tyr Ala Ser Arg Ser Ser Tyr Tyr Ala Asp Gln Thr Leu Phe
    130                 135                 140
Gly Asn Leu Ala Gln Gly Tyr Val Ser Ala Asn Asp Phe His Pro Ala
145                 150                 155                 160
Gly Cys Ile Ser Asp Trp Asn Asp Pro Gly His Val Gln Tyr Trp Arg
                165                 170                 175
Leu Cys Gly Ala Asp Gly Asp Val Gly Leu Pro Asp Leu Asp Pro Asn
            180                 185                 190
Asn Trp Val Val Ser Gln Gln Arg Leu Tyr Leu Lys Ala Leu Lys Asp
        195                 200                 205
Met Gly Ile Lys Gly Phe Arg Ile Asp Ala Val Lys His Met Ser Gln
    210                 215                 220
Tyr Gln Ile Asp Gln Val Phe Thr Ser Glu Ile Thr Ala Asn Met His
225                 230                 235                 240
Val Phe Gly Glu Val Ile Thr Ser Gly Gly Ala Gly Asn Ser Gly Tyr
                245                 250                 255
Glu Ser Phe Leu Ala Pro Tyr Leu Asn Asn Thr Asn His Ser Ala Tyr
            260                 265                 270
Asp Phe Pro Leu Phe Ala Ser Ile Arg Ser Ala Phe Ser Met Gly Gly
        275                 280                 285
Gly Leu Asn Gln Leu His Asp Pro Lys Ala Tyr Gly Gln Ala Leu Asp
    290                 295                 300
Asp Asn Arg Ser Ile Thr Phe Ala Ile Thr His Asp Ile Pro Thr Asn
305                 310                 315                 320
Asp Gly Phe Arg Tyr Gln Ile Met Asp Pro Gln Asp Glu Gln Leu Ala
                325                 330                 335
Tyr Ala Tyr Ile Leu Gly Lys Asp Gly Gly Thr Pro Leu Ile Tyr Ser
            340                 345                 350
Asp Asp Leu Pro Asp Ser Glu Asp Lys Asp Asn Gly Arg Trp Gly Asn
        355                 360                 365
Val Trp Asn Ser Ser Thr Met Lys Asn Met Leu Ser Phe His Asn Ala
    370                 375                 380
Met Gln Gly Lys Thr Met Thr Met Ile Ser Ser Asp His Cys Thr Leu
385                 390                 395                 400
Leu Phe Lys Arg Gly Lys Glu Gly Val Val Gly Ile Asn Lys Cys Gly
                405                 410                 415
Glu Thr Arg Gly Val Thr Val Asp Thr Tyr Gln His Glu Phe Asn Trp
            420                 425                 430
His Val Gln Tyr Lys Asp Val Leu Ser Ser Ala Thr Glu Thr Val Thr
        435                 440                 445
Ser Arg Tyr His Thr Phe Asn Leu Pro Pro Arg Ser Ala Arg Met Phe
    450                 455                 460
Lys Leu
```

465

<210> 143
<211> 1422
<212> DNA
<213> Environmental

<400> 143
atgccaaaga gcacttttac caaatccata acaaaatcac ttcttgctac ttccgttgtt 60
gtaagcttat tgcctgccta cgcacaggcc gacactatct tgcatgcctt taactggaaa 120
tacagcgaca ttacccgcca agcagagcaa attgcgcaag ctggttataa aaaagtactg 180
atttcaccgc cgctgaagtc cacaggccca caatggtggg cacgttacca accacaggac 240
attcgagtga ttgactcccc tgtcggcaac aagcaagatt tacaagccct cattgcagcc 300
ttaaaggcac aaggcgttga agtatacgca gacatcgtac tcaaccacat ggccaacgaa 360
agctggaaac gagacgatct gaactacccg ggaagtgatt tacttaccca atacagccaa 420
aatatggctt acatgaacca gcaaaaattg tttggagatt tagagcaaaa tcagttctct 480
gccaatgatt ttcacccggc tggctgcatt actgattgga gtaacccggg gcatgttcaa 540
tactggcgct tatgtggtgg taatggtgac actgggttac ctgatcttga tcctaactcg 600
tgggtgatcg atcaacaaaa acgttattta cgtgctttga aagacatggg aataaagggc 660
ttccgagttg atgcggtaaa acacatgagc gattaccaaa tcaaccaagt gtttacgcca 720
gacatcatcg caggcttaca tgtatttggt gaagtgatca ccagtggtgg caagggcagc 780
aatgactacc actcttttct ggaaccgtat ttaaataaca ccaatcacgc cgcgtatgac 840
ttcccgctat ttgcctctat ccgaaatgca tttagttatc atggcagctt gtctcaatta 900
catgatccac aagcttacgg gcaagcactt cctaacgaca gagccattac tttcaccatc 960
actcacgaca ttccaaccaa tgatggtttc cgttaccaaa tcatggatcc aaccagtgaa 1020
aaactcgcgt acgcgtacat tctaggcaaa gatgggggta gcccacttat ctatagcgat 1080
gctttagacc caagtgaaga taaagataag ggccgctggc gtgatgtatg gaaccaagaa 1140
tacatggtta acatgatcag cttccacaac aaggtgcaag gtaaaagcat ggaggtcatg 1200
tacagcgatc aatgcttgct ggtctttaaa cgtgaaaaac aaggcttagt cggtattaat 1260
aagtgcgctg aaagccgtac ctacaccata gatacccatc gttttgaatt taactggtac 1320
caaccgtaca acgacacatt aagccagcac agcgagacct ttagcagccg ttatcatgct 1380
ctgaccattc cggcgcaaac agcacgaatg ttggcgctat aa 1422

<210> 144
<211> 473
<212> PRT
<213> Environmental

<400> 144
Met Pro Lys Ser Thr Phe Thr Lys Ser Ile Thr Lys Ser Leu Leu Ala
1 5 10 15
Thr Ser Val Val Val Ser Leu Leu Pro Ala Tyr Ala Gln Ala Asp Thr
20 25 30
Ile Leu His Ala Phe Asn Trp Lys Tyr Ser Asp Ile Thr Arg Gln Ala
35 40 45
Glu Gln Ile Ala Gln Ala Gly Tyr Lys Lys Val Leu Ile Ser Pro Pro
50 55 60
Leu Lys Ser Thr Gly Pro Gln Trp Trp Ala Arg Tyr Gln Pro Gln Asp
65 70 75 80
Ile Arg Val Ile Asp Ser Pro Val Gly Asn Lys Gln Asp Leu Gln Ala
85 90 95
Leu Ile Ala Ala Leu Lys Ala Gln Gly Val Glu Val Tyr Ala Asp Ile
100 105 110
Val Leu Asn His Met Ala Asn Glu Ser Trp Lys Arg Asp Asp Leu Asn
115 120 125
Tyr Pro Gly Ser Asp Leu Leu Thr Gln Tyr Ser Gln Asn Met Ala Tyr
130 135 140

```
Met Asn Gln Gln Lys Leu Phe Gly Asp Leu Glu Gln Asn Gln Phe Ser
145                 150                 155                 160
Ala Asn Asp Phe His Pro Ala Gly Cys Ile Thr Asp Trp Ser Asn Pro
                165                 170                 175
Gly His Val Gln Tyr Trp Arg Leu Cys Gly Gly Asn Gly Asp Thr Gly
            180                 185                 190
Leu Pro Asp Leu Asp Pro Asn Ser Trp Val Ile Asp Gln Gln Lys Arg
        195                 200                 205
Tyr Leu Arg Ala Leu Lys Asp Met Gly Ile Lys Gly Phe Arg Val Asp
    210                 215                 220
Ala Val Lys His Met Ser Asp Tyr Gln Ile Asn Gln Val Phe Thr Pro
225                 230                 235                 240
Asp Ile Ile Ala Gly Leu His Val Phe Gly Glu Val Ile Thr Ser Gly
                245                 250                 255
Gly Lys Gly Ser Asn Asp Tyr His Ser Phe Leu Glu Pro Tyr Leu Asn
            260                 265                 270
Asn Thr Asn His Ala Ala Tyr Asp Phe Pro Leu Phe Ala Ser Ile Arg
        275                 280                 285
Asn Ala Phe Ser Tyr His Gly Ser Leu Ser Gln Leu His Asp Pro Gln
    290                 295                 300
Ala Tyr Gly Gln Ala Leu Pro Asn Asp Arg Ala Ile Thr Phe Thr Ile
305                 310                 315                 320
Thr His Asp Ile Pro Thr Asn Asp Gly Phe Arg Tyr Gln Ile Met Asp
                325                 330                 335
Pro Thr Ser Glu Lys Leu Ala Tyr Ala Tyr Ile Leu Gly Lys Asp Gly
            340                 345                 350
Gly Ser Pro Leu Ile Tyr Ser Asp Ala Leu Asp Pro Ser Glu Asp Lys
        355                 360                 365
Asp Lys Gly Arg Trp Arg Asp Val Trp Asn Gln Glu Tyr Met Val Asn
    370                 375                 380
Met Ile Ser Phe His Asn Lys Val Gln Gly Lys Ser Met Glu Val Met
385                 390                 395                 400
Tyr Ser Asp Gln Cys Leu Leu Val Phe Lys Arg Glu Lys Gln Gly Leu
                405                 410                 415
Val Gly Ile Asn Lys Cys Ala Glu Ser Arg Thr Tyr Thr Ile Asp Thr
            420                 425                 430
His Arg Phe Glu Phe Asn Trp Tyr Gln Pro Tyr Asn Asp Thr Leu Ser
        435                 440                 445
Gln His Ser Glu Thr Phe Ser Ser Arg Tyr His Ala Leu Thr Ile Pro
    450                 455                 460
Ala Gln Thr Ala Arg Met Leu Ala Leu
465                 470
```

<210> 145
<211> 1542
<212> DNA
<213> Environmental

<400> 145

```
atgttgaaaa ggattacggt agtctgttta ttatttattt tgctttttcc taatatatat      60
gggaggaata aggcggaagc agcaacgata aataatggaa cattaatgca gtattttgag     120
tggtacgctc cgaatgatgg gaatcattgg aatcgtttgc gttatgatgc tgaaagttta     180
gctcataagg gaatcacatc tgtatggata ccacctgcat ataaagggac ttcgcaaaat     240
gatgtagggt atggggccta tgatttatac gatttagggg agttcaatca aaaaggaacg     300
gtgcggacga aatatgggac aaaggcacag ttgaaatctg caattgacgc tttacataag     360
caaaacatcg acgtatacgg tgatgtagtt atgaatcata aaggtggggc tgattatact     420
gaaaccgtaa cagctgttga ggtagaccgt aacaatcgaa atattgaagt atcaggtgat     480
```

```
tatgaaatta gtgcgtggac gggttttaac tttccagggc gcagagatgc ttattctaat     540
ttcaaatgga aatggtatca ttttgacgga acggattggg atgaaggaag gaaattaaac     600
cgaatttata aatttagggg tataggtaaa gcgtgggact gggaagtgtc tagcgaaaat     660
ggaaattatg attatttgat gtatgcagat cttgattttg atcatccaga tgttgcgaat     720
gaaatgaaaa gttggggaac gtggtatgcg aatgaattaa atttagatgg atttcgttta     780
gatgctgtta aacatattga tcatgaatat ttacgcgatt gggtaaatca tgtcagacag     840
caaacgggga aagaaatgtt tacggtggct gaatattggc aaaatgatat ccagacttta     900
aacaattatt tggcgaaagt caattataat caatctgtat ttgatgcacc gcttcattac     960
aattttcatt atgcttcaac aggaaatggg aattatgata tgagaaatat tttaaatgga    1020
acagtaatga aaaatcatcc tgcactcgca gttactctcg ttgagaatca tgattctcaa    1080
cctgggcaat cattggaatc tgtagtaagt ccgtggttta agccgctggc atatgcattt    1140
attttaactc gtgcagaggg ctatccttca gtttttttatg gtgattacta tgggacaagc    1200
ggaaatagta gttatgaaat tccagcgtta aaagataaaa ttgatccaat tttgacggca    1260
cgaaaaaact ttgcatatgg tacgcagcgt gattatttag accatccaga tgtgattggc    1320
tggacaagag aaggagatag tgtacatgct aagtctggtt tagcggcatt aatctccgat    1380
ggaccaggag gatcaaagtg gatggatgtt ggaaagaata acgctgggga agtatggtac    1440
gatattacgg gtaatcaaac aaatactgta acaattaata aagatggatc ggggcaattc    1500
catgtaagtg gaggctctgt ttctatatat gttcaacagt aa                       1542
```

<210> 146
<211> 513
<212> PRT
<213> Environmental

<400> 146

```
Met Leu Lys Arg Ile Thr Val Val Cys Leu Leu Phe Ile Leu Leu Phe
 1               5                  10                  15
Pro Asn Ile Tyr Gly Arg Asn Lys Ala Glu Ala Ala Thr Ile Asn Asn
            20                  25                  30
Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Ala Pro Asn Asp Gly Asn
        35                  40                  45
His Trp Asn Arg Leu Arg Tyr Asp Ala Glu Ser Leu Ala His Lys Gly
    50                  55                  60
Ile Thr Ser Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln Asn
65                  70                  75                  80
Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn
                85                  90                  95
Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln Leu Lys
            100                 105                 110
Ser Ala Ile Asp Ala Leu His Lys Gln Asn Ile Asp Val Tyr Gly Asp
        115                 120                 125
Val Val Met Asn His Lys Gly Gly Ala Asp Tyr Thr Glu Thr Val Thr
    130                 135                 140
Ala Val Glu Val Asp Arg Asn Asn Arg Asn Ile Glu Val Ser Gly Asp
145                 150                 155                 160
Tyr Glu Ile Ser Ala Trp Thr Gly Phe Asn Phe Pro Gly Arg Arg Asp
                165                 170                 175
Ala Tyr Ser Asn Phe Lys Trp Lys Trp Tyr His Phe Asp Gly Thr Asp
            180                 185                 190
Trp Asp Glu Gly Arg Lys Leu Asn Arg Ile Tyr Lys Phe Arg Gly Ile
        195                 200                 205
Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn Tyr Asp
    210                 215                 220
Tyr Leu Met Tyr Ala Asp Leu Asp Phe Asp His Pro Asp Val Ala Asn
225                 230                 235                 240
Glu Met Lys Ser Trp Gly Thr Trp Tyr Ala Asn Glu Leu Asn Leu Asp
                245                 250                 255
```

```
Gly Phe Arg Leu Asp Ala Val Lys His Ile Asp His Glu Tyr Leu Arg
            260                 265                 270
Asp Trp Val Asn His Val Arg Gln Gln Thr Gly Lys Glu Met Phe Thr
        275                 280                 285
Val Ala Glu Tyr Trp Gln Asn Asp Ile Gln Thr Leu Asn Asn Tyr Leu
    290                 295                 300
Ala Lys Val Asn Tyr Asn Gln Ser Val Phe Asp Ala Pro Leu His Tyr
305                 310                 315                 320
Asn Phe His Tyr Ala Ser Thr Gly Asn Gly Asn Tyr Asp Met Arg Asn
                325                 330                 335
Ile Leu Asn Gly Thr Val Met Lys Asn His Pro Ala Leu Ala Val Thr
            340                 345                 350
Leu Val Glu Asn His Asp Ser Gln Pro Gly Gln Ser Leu Glu Ser Val
        355                 360                 365
Val Ser Pro Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
    370                 375                 380
Ala Glu Gly Tyr Pro Ser Val Phe Tyr Gly Asp Tyr Tyr Gly Thr Ser
385                 390                 395                 400
Gly Asn Ser Ser Tyr Glu Ile Pro Ala Leu Lys Asp Lys Ile Asp Pro
                405                 410                 415
Ile Leu Thr Ala Arg Lys Asn Phe Ala Tyr Gly Thr Gln Arg Asp Tyr
            420                 425                 430
Leu Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Ser Val
        435                 440                 445
His Ala Lys Ser Gly Leu Ala Ala Leu Ile Ser Asp Gly Pro Gly Gly
    450                 455                 460
Ser Lys Trp Met Asp Val Gly Lys Asn Asn Ala Gly Glu Val Trp Tyr
465                 470                 475                 480
Asp Ile Thr Gly Asn Gln Thr Asn Thr Val Thr Ile Asn Lys Asp Gly
                485                 490                 495
Ser Gly Gln Phe His Val Ser Gly Gly Ser Val Ser Ile Tyr Val Gln
            500                 505                 510
Gln
```

<210> 147
<211> 2343
<212> DNA
<213> Environmental

<400> 147

```
atgagcttaa ataactttaa ggtaaaactg cttagttttg ctgtgtcttc tgctgtattg      60
tcactggctc caaatttagc caatgctgca aattttgaaa gtgagatggt gataatccat     120
ccgtttcagt ggacatatga caatatagca aaagagtgta cagagtacct tggtccagcc     180
ggatttgacg gtgtacagat ttcccagcca gcggaacata agcgggctga aggagtatgg     240
tgggccgtat atcagccggt taattataag aattttacaa ccatgaccgg taacgaggag     300
cagcttaagg caatgatcaa gacctgtaat gatgcaggtg ttaaggtgtt cgctgacgct     360
gttttcaacc aaaaggctac agacggtgta ggctggggcg gttcaacttg gagttataag     420
aactaccctg acggattctc cggatcagat ttccatggag actgttccat tgacaaaagc     480
tatactgatg caaataatgt cagaacctgt gcactctcag gtatgccgga cgttgccaca     540
gataactccg ctactcagga aaagattgca gattacctcg cttctttaat gaatatgggg     600
gtctatggtt tccgtattga cgctgcaaag cacatgggat acaacgatat caactccatt     660
ctttcaaaaa ctgcacagaa gactggaaga agacctcctg catatctgga agtaatcgga     720
gccggtaacg aagctgccga cattcagccg gacaagtata cctttattga gaatgcggtt     780
gtaactgact tcggttatgt ctgggatgca aatgagagtt tcggaaaggg taattacggt     840
aaggcactgg aactcagtac ctggctcggt gcaaattcag aaacattcgt aaacaatcat     900
gatgatgaat ggggcagatg ctcagccggt agctgctcaa tgaaaactca gaattatgct     960
```

```
gattataatc tggctcagtc ctggcttgct gtatggcctg taggtacagt aagacagata    1020
tattccggtt attcattccc tgtaaaagat aatgatcctt atcgcgtcag tgatgcaact    1080
catgatcagg gcgggcctct tggtgccgac cgctgtgaag gtggctggtt gtgtcagcac    1140
cgtgtgtcct tcgttctcaa ttccccaaga tttgcgagag ctaccagagg tactgctgta    1200
tcaaccaagg gatttgacaa tggtgctttg tggtttaaca gaggaagcaa aggtttttat    1260
gcacagaata ctaccaacag tcctataacc cagacattct ctgttgaagt acctgacgga    1320
aattactgtg atatcttagg aacatcagat cctaagagca atccatgcgg agcagacgtt    1380
gtcgtaagcg gcggtaaggc tacctttact attcctgcaa agacagctgt ggctatctgt    1440
acagactcag actggtgcgg caaggggttt gatccttgtg aaagtgatcc gaccggtgct    1500
gcctgtgttt gtaaggggga aaccaccgtt aatggtgtgt gcgtcagctg gtgtaatgcg    1560
cattcatcaa atgaggaatg cacctgtgta ttgaatccga atgatgccaa ctgtcaggct    1620
gatattgaac ctaccaaggg taaactctgt tacgccggta cttcaaacgg gtggaaacag    1680
gatcctttaa catataaccg taaaacaggt ttctggacta ttaatctgac tcttgacggt    1740
gcaggtgata ccagcggagc tcagcgcttc aaggttacag acggatgttc atggaccgga    1800
acagtttacg gttcttcagg tactgccgga aagttggatg taaatacatc atcaaccggc    1860
gatgaacctg tgtctcttgt tggtgattat gttctttcca ttaacgataa gaccatggaa    1920
tatacattca ccaaggcaga tgaagtaact aatcagccac cggttgcatc atttaccgcg    1980
acagttaacg gtctgaccgt ttcttttgcc aataattcat ccgaccctga gaatgatgaa    2040
ttaacctaca gctggaattt cggtaatggt aaaacatcat ccgagaaagc tcctagcata    2100
acctatgaag aatccggtaa gtatactgtt actttaaagg ttactgattc agctaataac    2160
actgatacat ttactaaaga tataactgta acagcacctt ctagtggcaa gtacttaaag    2220
gttgcagtca gaggttcgca tgataattac ggaactgatc tgttaaccaa gaacggttct    2280
gattggaccg gcgtctttga attctttgga tccactagtg tcgacctgca ggcgcgcgag    2340
ctc                                                                  2343
```

<210> 148
<211> 781
<212> PRT
<213> Environmental

<400> 148

```
Met Ser Leu Asn Asn Phe Lys Val Lys Leu Leu Ser Phe Ala Val Ser
 1               5                  10                  15
Ser Ala Val Leu Ser Leu Ala Pro Asn Leu Ala Asn Ala Ala Asn Phe
            20                  25                  30
Glu Ser Glu Met Val Ile Ile His Pro Phe Gln Trp Thr Tyr Asp Asn
        35                  40                  45
Ile Ala Lys Glu Cys Thr Glu Tyr Leu Gly Pro Ala Gly Phe Asp Gly
    50                  55                  60
Val Gln Ile Ser Gln Pro Ala Glu His Lys Arg Ala Glu Gly Val Trp
65                  70                  75                  80
Trp Ala Val Tyr Gln Pro Val Asn Tyr Lys Asn Phe Thr Thr Met Thr
                85                  90                  95
Gly Asn Glu Glu Gln Leu Lys Ala Met Ile Lys Thr Cys Asn Asp Ala
            100                 105                 110
Gly Val Lys Val Phe Ala Asp Ala Val Phe Asn Gln Lys Ala Thr Asp
        115                 120                 125
Gly Val Gly Trp Gly Gly Ser Thr Trp Ser Tyr Lys Asn Tyr Pro Asp
    130                 135                 140
Gly Phe Ser Gly Ser Asp Phe His Gly Asp Cys Ser Ile Asp Lys Ser
145                 150                 155                 160
Tyr Thr Asp Ala Asn Asn Val Arg Thr Cys Ala Leu Ser Gly Met Pro
                165                 170                 175
Asp Val Ala Thr Asp Asn Ser Ala Thr Gln Glu Lys Ile Ala Asp Tyr
            180                 185                 190
Leu Ala Ser Leu Met Asn Met Gly Val Tyr Gly Phe Arg Ile Asp Ala
        195                 200                 205
```

```
Ala Lys His Met Gly Tyr Asn Asp Ile Asn Ser Ile Leu Ser Lys Thr
    210                 215                 220
Ala Gln Lys Thr Gly Arg Arg Pro Pro Ala Tyr Leu Glu Val Ile Gly
225                 230                 235                 240
Ala Gly Asn Glu Ala Ala Asp Ile Gln Pro Asp Lys Tyr Thr Phe Ile
                245                 250                 255
Glu Asn Ala Val Val Thr Asp Phe Gly Tyr Val Trp Asp Ala Asn Glu
            260                 265                 270
Ser Phe Gly Lys Gly Asn Tyr Gly Lys Ala Leu Glu Leu Ser Thr Trp
        275                 280                 285
Leu Gly Ala Asn Ser Glu Thr Phe Val Asn Asn His Asp Asp Glu Trp
    290                 295                 300
Gly Arg Cys Ser Ala Gly Ser Cys Ser Met Lys Thr Gln Asn Tyr Ala
305                 310                 315                 320
Asp Tyr Asn Leu Ala Gln Ser Trp Leu Ala Val Trp Pro Val Gly Thr
                325                 330                 335
Val Arg Gln Ile Tyr Ser Gly Tyr Ser Phe Pro Val Lys Asp Asn Asp
            340                 345                 350
Pro Tyr Arg Val Ser Asp Ala Thr His Asp Gln Gly Gly Pro Leu Gly
        355                 360                 365
Ala Asp Arg Cys Glu Gly Gly Trp Leu Cys Gln His Arg Val Ser Phe
    370                 375                 380
Val Leu Asn Ser Pro Arg Phe Ala Arg Ala Thr Arg Gly Thr Ala Val
385                 390                 395                 400
Ser Thr Lys Gly Phe Asp Asn Gly Ala Leu Trp Phe Asn Arg Gly Ser
                405                 410                 415
Lys Gly Phe Tyr Ala Gln Asn Thr Thr Asn Ser Pro Ile Thr Gln Thr
            420                 425                 430
Phe Ser Val Glu Val Pro Asp Gly Asn Tyr Cys Asp Ile Leu Gly Thr
        435                 440                 445
Ser Asp Pro Lys Ser Asn Pro Cys Gly Ala Asp Val Val Val Ser Gly
    450                 455                 460
Gly Lys Ala Thr Phe Thr Ile Pro Ala Lys Thr Ala Val Ala Ile Cys
465                 470                 475                 480
Thr Asp Ser Asp Trp Cys Gly Lys Gly Val Asp Pro Cys Glu Ser Asp
                485                 490                 495
Pro Thr Gly Ala Ala Cys Val Cys Lys Gly Glu Thr Thr Val Asn Gly
            500                 505                 510
Val Cys Val Ser Trp Cys Asn Ala His Ser Ser Asn Glu Glu Cys Thr
        515                 520                 525
Cys Val Leu Asn Pro Asn Asp Ala Asn Cys Gln Ala Asp Ile Glu Pro
    530                 535                 540
Thr Lys Gly Lys Leu Cys Tyr Ala Gly Thr Ser Asn Gly Trp Lys Gln
545                 550                 555                 560
Asp Pro Leu Thr Tyr Asn Arg Lys Thr Gly Phe Trp Thr Ile Asn Leu
                565                 570                 575
Thr Leu Asp Gly Ala Gly Asp Thr Ser Gly Ala Gln Arg Phe Lys Val
            580                 585                 590
Thr Asp Gly Cys Ser Trp Thr Gly Thr Val Tyr Gly Ser Ser Gly Thr
        595                 600                 605
Ala Gly Lys Leu Asp Val Asn Thr Ser Ser Thr Gly Asp Glu Pro Val
    610                 615                 620
Ser Leu Val Gly Asp Tyr Val Leu Ser Ile Asn Asp Lys Thr Met Glu
625                 630                 635                 640
Tyr Thr Phe Thr Lys Ala Asp Glu Val Thr Asn Gln Pro Pro Val Ala
                645                 650                 655
Ser Phe Thr Ala Thr Val Asn Gly Leu Thr Val Ser Phe Ala Asn Asn
```

```
            660                 665                 670
Ser Ser Asp Pro Glu Asn Asp Glu Leu Thr Tyr Ser Trp Asn Phe Gly
        675                 680                 685
Asn Gly Lys Thr Ser Ser Glu Lys Ala Pro Ser Ile Thr Tyr Glu Glu
    690                 695                 700
Ser Gly Lys Tyr Thr Val Thr Leu Lys Val Thr Asp Ser Ala Asn Asn
705                 710                 715                 720
Thr Asp Thr Phe Thr Lys Asp Ile Thr Val Thr Ala Pro Ser Ser Gly
                725                 730                 735
Lys Tyr Leu Lys Val Ala Val Arg Gly Ser His Asp Asn Tyr Gly Thr
            740                 745                 750
Asp Leu Leu Thr Lys Asn Gly Ser Asp Trp Thr Gly Val Phe Glu Phe
        755                 760                 765
Phe Gly Ser Thr Ser Val Asp Leu Gln Ala Arg Glu Leu
    770                 775                 780
```

<210> 149
<211> 2502
<212> DNA
<213> Environmental

<400> 149

```
atgatcttaa gtaattttaa ggtaaaactt cttagttttg ctgtgtcttc tgctgtactg      60
acactggctg caaatgtcgc caatgccaag aattatgaaa gtgaaatggt tattattcat     120
ccatttcagt ggacatatga caatatagca aaagaatgta ctgagtatct gggacctgcg     180
ggatttgacg gggtgcagat ttcccaggcg gctgagcata aagatgccgg tggtgcatgg     240
tggggtacct accagcctgt aaacttcaag agttttacta ccatggttgg taatgaagaa     300
cagcttagag caatgattaa aacctgtaac gaggcaggtg ttaaggtctt tgccgatgcc     360
gtgattaatc agaaagccgg cgacggtgta ggtataggtg gttcaacttt cggaaattat     420
aattatcctg acggatttac cagtgatgat tttcatcata ataactgcag tataggtaat     480
aattattcag atgcatgggt agtaagattc tgtgacctca gtggcatgcc ggatatagca     540
actgataacg acagtaccag aaataagatt gctgattact tcgccagcct tatgaatatg     600
ggggtatacg gattccgtat tgatgctgcc aagcacttta gctatgatga tatagacgct     660
attgtagaga aaacagcaac caaagcaggc aggagacctc ctgtctatat ggaggttatc     720
ggtaatccgg gtcaagaggc ggatgatatc cagccgaaca agtatacatg gattgataat     780
gccgttgtaa cagattttac ttatgctaat agcatgcata atatttttaa cggaagcggt     840
tatgccaagg ctttgaacat ggggctaggg catgttgatg ctgaaaatgc cgaagtcttt     900
ataagtaatc atgataatga atggggaaga aagtctgccg gttcctgctc aataagaacc     960
cagaataatc cggattacca tctggctcag tcctggctcg cagtttggcc tttaggcaag    1020
gttagacaga tttattctgc atatcagttc ccggtctttg aagatagttg tgagcgggtc    1080
agtcagcaag cccatgatca gggcggtcct atcggggcag cccgctgtga aggtggctgg    1140
ttgtgtcagc accgtgtacc gtttgtgctc aattctccta gatttgcaag agcaaccaga    1200
gggacagtcg ttactactaa aggttttgat gacggagctt tgtggtttaa cagaggaagc    1260
aagggcttct atgcccagaa tactaccggc agttctataa ctcatacatt ctcagttgaa    1320
ttacctgatg gaaattactg tgatatcctt ggagcaaccg atccgaagaa taatccttgc    1380
ggagcggatg tcactgtaag cggaggtaaa gcaaccttta ccattccggc aaagaccgcc    1440
gtagctatct gtactgatga aaagtggtgt ggcaaggggg ttgacccttg tgaaagcgat    1500
cctaccggtt ccgcctgtgt atgtaagggt gaaaccacag ttaacggcgt atgtgtaagc    1560
tggtgtaatg ctcactcatc taatgaagaa tgtgcctgtg tgctaaatcc taatgacgct    1620
gagtgtcagg ccgacattga gccgaccaag ggtaaactct gctatgtagg tacctccaac    1680
aagtggactc aggaaccttt aacctataat cgcaagaccg gtttctggac tctcaacgtt    1740
gaacttgacg gtaaggggga taccagcggg gcgcagcgct ttaaagttac cgacggctgt    1800
tcatggcagg gtactgttta cggttcatca ggagtagaag gcagacttga cgtaaatact    1860
tcagccaccg gagatgaacc ggtttcactg acaggtaaat atgttctttc cataaatgat    1920
aagaccatgg aatacacatt cattcctgca ggcagtggaa acaagcctcc ggttgcgtca    1980
tttactccga ctgttaaaga tctgactgta tcttttgtca ataattcatc cgaccctgag    2040
aatgatgaat taacctacag ctggaatttc ggtaacggta aaacctcatc tgaaaagaat    2100
```

```
ccgagtgtta catatgataa agccggtaaa tatactgttt cactcaaagt aaccgatact    2160
gcaaacaaca ctgataccaa aacactggaa atcgatttaa catctcctgt taacggaaaa    2220
tattccaagg ttgcagtcag aggttcacat gataactacg gaacaaatct gttaaccagg    2280
aatggttcag aatggaccgg tatctttgaa ttcagtaaga caaccaaatt caagcttgaa    2340
gctctgcctc ctgcagctga ccagtgtatc ttcctcggcg gtaatcgagg tgaggcattg    2400
actgcctccg gtggatttat atctcttcct gccggaaggt atactataaa gtttaatgag    2460
gaaagcaagg ttcttactgc aggcgatgtt gactgcaccg gg                       2502
```

<210> 150
<211> 834
<212> PRT
<213> Environmental

<400> 150

```
Met Ile Leu Ser Asn Phe Lys Val Lys Leu Leu Ser Phe Ala Val Ser
 1               5                  10                  15
Ser Ala Val Leu Thr Leu Ala Ala Asn Val Ala Asn Ala Lys Asn Tyr
            20                  25                  30
Glu Ser Glu Met Val Ile Ile His Pro Phe Gln Trp Thr Tyr Asp Asn
        35                  40                  45
Ile Ala Lys Glu Cys Thr Glu Tyr Leu Gly Pro Ala Gly Phe Asp Gly
    50                  55                  60
Val Gln Ile Ser Gln Ala Ala Glu His Lys Asp Ala Gly Gly Ala Trp
65                  70                  75                  80
Trp Gly Thr Tyr Gln Pro Val Asn Phe Lys Ser Phe Thr Thr Met Val
                85                  90                  95
Gly Asn Glu Glu Gln Leu Arg Ala Met Ile Lys Thr Cys Asn Glu Ala
            100                 105                 110
Gly Val Lys Val Phe Ala Asp Ala Val Ile Asn Gln Lys Ala Gly Asp
        115                 120                 125
Gly Val Gly Ile Gly Gly Ser Thr Phe Gly Asn Tyr Asn Tyr Pro Asp
    130                 135                 140
Gly Phe Thr Ser Asp Asp Phe His His Asn Asn Cys Ser Ile Gly Asn
145                 150                 155                 160
Asn Tyr Ser Asp Ala Trp Val Val Arg Phe Cys Asp Leu Ser Gly Met
                165                 170                 175
Pro Asp Ile Ala Thr Asp Asn Asp Ser Thr Arg Asn Lys Ile Ala Asp
            180                 185                 190
Tyr Phe Ala Ser Leu Met Asn Met Gly Val Tyr Gly Phe Arg Ile Asp
        195                 200                 205
Ala Ala Lys His Phe Ser Tyr Asp Asp Ile Asp Ala Ile Val Glu Lys
    210                 215                 220
Thr Ala Thr Lys Ala Gly Arg Arg Pro Pro Val Tyr Met Glu Val Ile
225                 230                 235                 240
Gly Asn Pro Gly Gln Glu Ala Asp Asp Ile Gln Pro Asn Lys Tyr Thr
                245                 250                 255
Trp Ile Asp Asn Ala Val Val Thr Asp Phe Thr Tyr Ala Asn Ser Met
            260                 265                 270
His Asn Ile Phe Asn Gly Ser Gly Tyr Ala Lys Ala Leu Asn Met Gly
        275                 280                 285
Leu Gly His Val Asp Ala Glu Asn Ala Glu Val Phe Ile Ser Asn His
    290                 295                 300
Asp Asn Glu Trp Gly Arg Lys Ser Ala Gly Ser Cys Ser Ile Arg Thr
305                 310                 315                 320
Gln Asn Asn Pro Asp Tyr His Leu Ala Gln Ser Trp Leu Ala Val Trp
                325                 330                 335
Pro Leu Gly Lys Val Arg Gln Ile Tyr Ser Ala Tyr Gln Phe Pro Val
```

```
            340                 345                 350
Phe Glu Asp Ser Cys Glu Arg Val Ser Gln Gln Ala His Asp Gln Gly
        355                 360                 365
Gly Pro Ile Gly Ala Ala Arg Cys Glu Gly Gly Trp Leu Cys Gln His
    370                 375                 380
Arg Val Pro Phe Val Leu Asn Ser Pro Arg Phe Ala Arg Ala Thr Arg
385                 390                 395                 400
Gly Thr Val Val Thr Thr Lys Gly Phe Asp Asp Gly Ala Leu Trp Phe
                405                 410                 415
Asn Arg Gly Ser Lys Gly Phe Tyr Ala Gln Asn Thr Thr Gly Ser Ser
            420                 425                 430
Ile Thr His Thr Phe Ser Val Glu Leu Pro Asp Gly Asn Tyr Cys Asp
        435                 440                 445
Ile Leu Gly Ala Thr Asp Pro Lys Asn Asn Pro Cys Gly Ala Asp Val
    450                 455                 460
Thr Val Ser Gly Gly Lys Ala Thr Phe Thr Ile Pro Ala Lys Thr Ala
465                 470                 475                 480
Val Ala Ile Cys Thr Asp Glu Lys Trp Cys Gly Lys Gly Val Asp Pro
                485                 490                 495
Cys Glu Ser Asp Pro Thr Gly Ser Ala Cys Val Cys Lys Gly Glu Thr
            500                 505                 510
Thr Val Asn Gly Val Cys Val Ser Trp Cys Asn Ala His Ser Ser Asn
        515                 520                 525
Glu Glu Cys Ala Cys Val Leu Asn Pro Asn Asp Ala Glu Cys Gln Ala
    530                 535                 540
Asp Ile Glu Pro Thr Lys Gly Lys Leu Cys Tyr Val Gly Thr Ser Asn
545                 550                 555                 560
Lys Trp Thr Gln Glu Pro Leu Thr Tyr Asn Arg Lys Thr Gly Phe Trp
                565                 570                 575
Thr Leu Asn Val Glu Leu Asp Gly Lys Gly Asp Thr Ser Gly Ala Gln
            580                 585                 590
Arg Phe Lys Val Thr Asp Gly Cys Ser Trp Gln Gly Thr Val Tyr Gly
        595                 600                 605
Ser Ser Gly Val Glu Gly Arg Leu Asp Val Asn Thr Ser Ala Thr Gly
    610                 615                 620
Asp Glu Pro Val Ser Leu Thr Gly Lys Tyr Val Leu Ser Ile Asn Asp
625                 630                 635                 640
Lys Thr Met Glu Tyr Thr Phe Ile Pro Ala Gly Ser Gly Asn Lys Pro
                645                 650                 655
Pro Val Ala Ser Phe Thr Pro Thr Val Lys Asp Leu Thr Val Ser Phe
            660                 665                 670
Val Asn Asn Ser Ser Asp Pro Glu Asn Asp Glu Leu Thr Tyr Ser Trp
        675                 680                 685
Asn Phe Gly Asn Gly Lys Thr Ser Ser Glu Lys Asn Pro Ser Val Thr
    690                 695                 700
Tyr Asp Lys Ala Gly Lys Tyr Thr Val Ser Leu Lys Val Thr Asp Thr
705                 710                 715                 720
Ala Asn Asn Thr Asp Thr Lys Thr Leu Glu Ile Asp Leu Thr Ser Pro
                725                 730                 735
Val Asn Gly Lys Tyr Ser Lys Val Ala Val Arg Gly Ser His Asp Asn
            740                 745                 750
Tyr Gly Thr Asn Leu Leu Thr Arg Asn Gly Ser Glu Trp Thr Gly Ile
        755                 760                 765
Phe Glu Phe Ser Lys Thr Thr Lys Phe Lys Leu Glu Ala Leu Pro Pro
    770                 775                 780
Ala Ala Asp Gln Cys Ile Phe Leu Gly Gly Asn Arg Gly Glu Ala Leu
785                 790                 795                 800
```

```
Thr Ala Ser Gly Gly Phe Ile Ser Leu Pro Ala Gly Arg Tyr Thr Ile
                805                 810                 815
Lys Phe Asn Glu Glu Ser Lys Val Leu Thr Ala Gly Asp Val Asp Cys
            820                 825                 830
Thr Gly
```

<210> 151
<211> 2112
<212> DNA
<213> Environmental

<400> 151

```
atgaaaacta ttctttcaac aatcatggtg atggcggctg cggctgccac caccgtagag      60
gctcaaggct ggccggaaaa ctacggcggc gtcatgttgc agggattcta ctgggattcc     120
tattcagcca ccaagtggac taaactggaa gcacaggctg acgagatctg caactatttc     180
tcgctggtat gggtaccaca gtcggcctat accggcagca gtacctccat gggctacgac     240
ccgctgtatt acttcgacca gcattcatcg ttcggcaccg aagagcagct acggtcgttc     300
atcagtacct acaagcagaa aggaactggc atcatagccg atgtagttgt caatcaccga     360
aagaatgtct caaactgggt ggatttcccg gccgagacct acaacggtgt aacctatcag     420
atggtaagca ccgacatcgt ttcgaacgat gacggcggaa aaacagccac ttgggcaaat     480
caaaacggct acagtctctc ctccaatgcc gacgaaggcg aaggctggga cggcatgcgc     540
gacctggacc acaagtcgca gaacgtgcag aaatcggttc ttgcctacac caaatatctg     600
gttgacgact taggctatac cggattccgc tacgatatgg taaagggatt tgacggatcg     660
catgtagccg actacaacac caatgccggc gtgcagttct ctgtcggcga tattgggac      720
ggcactgcat cgaaagttta cagttggatc aacagcacca aaaagagcga tgtgccgcag     780
tcggcagcct tcgacttcgc tttccgatac acctgccgcg atgccgtcaa caacaagaac     840
tgggcgaacc tgaagaacac ttccggtatc agcgatgccg attacaggcg ctattcggtt     900
acgtttgttg aaaatcacga tacggaatac cgttcagcta cggcttccca ggatcccatc     960
aagggtgata cggttgccct caatgcctgg atgctggcta tgccgggcac accttgtgtt    1020
ttcctgaaac attggaccga ctgcaaggaa gagatcaaga atctcatcga ggcacgtcgc    1080
ctggtcggta ttcacaacca gagcacctat gccgaatgga tgagcggtgc agcctacatc    1140
ggacgtaccg taacaggtac gaacggcacc ttacgtgttc tgtgcggctc ttatcagtat    1200
aatgtagccg ccaactacat tcagattctc tcaggcaaaa actataaata ctacgtactc    1260
aacacgctcg aggctccctg gatcgggaaa ggttccggct cgtacaccga aggtgaaacc    1320
gtaacggttc cgctcatcgc catatcggcc gatgccaatg ccaagctggt atataccacc    1380
gacggcacag accccaccgc aacctcaaca gccgtaacca gcggaacgga actgaccatc    1440
acttcggacg ccgtcctgaa ggttggtctg ctttccggcg gcatcgtcag gaacatacag    1500
agccgtacat tcaccttcca ggctgcaaac acctccgagt attacacagc caccatgcac    1560
gtatgcaacc agtccggagc tctcaatccg ctgtttgcct atgtttgggc aggaccggac    1620
aacgagcaga ttaacggcaa ctggccgggc accaagctca ccgctaccat taccgaaaac    1680
aaccttacct ggtacacgca gtcgttccag attccgaaga acgtggacta tgtcgtgaac    1740
tttgttttca ccacaaccgg cggcggtacg cagacagtgg atgttaccgg catgaaggcc    1800
gatgtctggt acattattaa cagtaccaag agcggcaaca agtacacggt aaccgacgtt    1860
acctcacagt attcttcgtt agaggccatc tttgatgaag aaaactccgg ctccttccct    1920
gtctatgacc tgcagggacg ccgcgtcagc gaaattagaa acaggacaat tatatcttca    1980
gaacggaaag aagatactca tcagataaac agaggttccg aaccattctc ctattatgaa    2040
aatcagacac ttagtaatct cagcactgct gggtttgggg ggcttgtaca ccatcagctg    2100
ctcctcgtcg gg                                                        2112
```

<210> 152
<211> 704
<212> PRT
<213> Environmental

<400> 152

```
Met Lys Thr Ile Leu Ser Thr Ile Met Val Met Ala Ala Ala Ala Ala
```

```
 1               5                  10                  15
Thr Thr Val Glu Ala Gln Gly Trp Pro Glu Asn Tyr Gly Gly Val Met
            20                  25                  30
Leu Gln Gly Phe Tyr Trp Asp Ser Tyr Ser Ala Thr Lys Trp Thr Lys
        35                  40                  45
Leu Glu Ala Gln Ala Asp Glu Ile Cys Asn Tyr Phe Ser Leu Val Trp
    50                  55                  60
Val Pro Gln Ser Ala Tyr Thr Gly Ser Ser Thr Ser Met Gly Tyr Asp
65                  70                  75                  80
Pro Leu Tyr Tyr Phe Asp Gln His Ser Ser Phe Gly Thr Glu Glu Gln
                85                  90                  95
Leu Arg Ser Phe Ile Ser Thr Tyr Lys Gln Lys Gly Thr Gly Ile Ile
            100                 105                 110
Ala Asp Val Val Val Asn His Arg Lys Asn Val Ser Asn Trp Val Asp
        115                 120                 125
Phe Pro Ala Glu Thr Tyr Asn Gly Val Thr Tyr Gln Met Val Ser Thr
    130                 135                 140
Asp Ile Val Ser Asn Asp Asp Gly Gly Lys Thr Ala Thr Trp Ala Asn
145                 150                 155                 160
Gln Asn Gly Tyr Ser Leu Ser Ser Asn Ala Asp Glu Gly Glu Gly Trp
                165                 170                 175
Asp Gly Met Arg Asp Leu Asp His Lys Ser Gln Asn Val Gln Lys Ser
            180                 185                 190
Val Leu Ala Tyr Thr Lys Tyr Leu Val Asp Asp Leu Gly Tyr Thr Gly
        195                 200                 205
Phe Arg Tyr Asp Met Val Lys Gly Phe Asp Gly Ser His Val Ala Asp
    210                 215                 220
Tyr Asn Thr Asn Ala Gly Val Gln Phe Ser Val Gly Glu Tyr Trp Asp
225                 230                 235                 240
Gly Thr Ala Ser Lys Val Tyr Ser Trp Ile Asn Ser Thr Lys Lys Ser
                245                 250                 255
Asp Val Pro Gln Ser Ala Ala Phe Asp Phe Ala Phe Arg Tyr Thr Cys
            260                 265                 270
Arg Asp Ala Val Asn Asn Lys Asn Trp Ala Asn Leu Lys Asn Thr Ser
        275                 280                 285
Gly Ile Ser Asp Ala Asp Tyr Arg Arg Tyr Ser Val Thr Phe Val Glu
    290                 295                 300
Asn His Asp Thr Glu Tyr Arg Ser Ala Thr Ala Ser Gln Asp Pro Ile
305                 310                 315                 320
Lys Gly Asp Thr Val Ala Leu Asn Ala Trp Met Leu Ala Met Pro Gly
                325                 330                 335
Thr Pro Cys Val Phe Leu Lys His Trp Thr Asp Cys Lys Glu Glu Ile
            340                 345                 350
Lys Asn Leu Ile Glu Ala Arg Arg Leu Val Gly Ile His Asn Gln Ser
        355                 360                 365
Thr Tyr Ala Glu Trp Met Ser Gly Ala Ala Tyr Ile Gly Arg Thr Val
    370                 375                 380
Thr Gly Thr Asn Gly Thr Leu Arg Val Leu Cys Gly Ser Tyr Gln Tyr
385                 390                 395                 400
Asn Val Ala Ala Asn Tyr Ile Gln Ile Leu Ser Gly Lys Asn Tyr Lys
                405                 410                 415
Tyr Tyr Val Leu Asn Thr Leu Glu Ala Pro Trp Ile Gly Lys Gly Ser
            420                 425                 430
Gly Ser Tyr Thr Glu Gly Glu Thr Val Thr Val Pro Leu Ile Ala Ile
        435                 440                 445
Ser Ala Asp Ala Asn Ala Lys Leu Val Tyr Thr Thr Asp Gly Thr Asp
    450                 455                 460
```

```
Pro Thr Ala Thr Ser Thr Ala Val Thr Ser Gly Thr Glu Leu Thr Ile
465                 470                 475                 480
Thr Ser Asp Ala Val Leu Lys Val Gly Leu Leu Ser Gly Gly Ile Val
                485                 490                 495
Arg Asn Ile Gln Ser Arg Thr Phe Thr Phe Gln Ala Ala Asn Thr Ser
            500                 505                 510
Glu Tyr Tyr Thr Ala Thr Met His Val Cys Asn Gln Ser Gly Ala Leu
        515                 520                 525
Asn Pro Leu Phe Ala Tyr Val Trp Ala Gly Pro Asp Asn Glu Gln Ile
    530                 535                 540
Asn Gly Asn Trp Pro Gly Thr Lys Leu Thr Ala Thr Ile Thr Glu Asn
545                 550                 555                 560
Asn Leu Thr Trp Tyr Thr Gln Ser Phe Gln Ile Pro Lys Asn Val Asp
                565                 570                 575
Tyr Val Val Asn Phe Val Phe Thr Thr Thr Gly Gly Gly Thr Gln Thr
            580                 585                 590
Val Asp Val Thr Gly Met Lys Ala Asp Val Trp Tyr Ile Ile Asn Ser
        595                 600                 605
Thr Lys Ser Gly Asn Lys Tyr Thr Val Thr Asp Val Thr Ser Gln Tyr
    610                 615                 620
Ser Ser Leu Glu Ala Ile Phe Asp Glu Glu Asn Ser Gly Ser Phe Pro
625                 630                 635                 640
Val Tyr Asp Leu Gln Gly Arg Arg Val Ser Glu Ile Arg Asn Arg Thr
                645                 650                 655
Ile Ile Ser Ser Glu Arg Lys Glu Asp Thr His Gln Ile Asn Arg Gly
            660                 665                 670
Ser Glu Pro Phe Ser Tyr Tyr Glu Asn Gln Thr Leu Ser Asn Leu Ser
        675                 680                 685
Thr Ala Gly Phe Gly Gly Leu Val His His Gln Leu Leu Leu Val Gly
    690                 695                 700
```

<210> 153
<211> 1620
<212> DNA
<213> Environmental

<400> 153

```
atgccttcaa ttaatgcaag cgattgcaaa aaaaagggag ataggagtat gaagaggaaa      60
aaatggactg cgttagcact atctttacca ctagttatga gcttatcaac aaacatacaa     120
gcagaaacat tacataataa taagggtcaa aaggcgcaaa caggaaataa agacggaatt     180
ttttatgaac tgtatgttaa ttctttttat gatactgata gcaatggaca tggtgattta     240
aaaggcgtca caaagaaact tgattattta aatgatggaa atccaagaac aaataatgat     300
cttcaaataa acggtatctg gatgatgcct attaacacct ctcctagtta tcacaaatat     360
gatgtaacag attactataa tatcgatcct cagtatggaa gtttacaaga tttccgtgaa     420
ctaacaacag aagcgcataa acgcaacgta aaggtagtaa tagatcttgt tattaatcat     480
acaagcagtg agcatccttg gtttgtcgat gcattaaaaa ataaaaacag taagtatcga     540
gattactata tttgggctga taaaaataca gacttaaatg aaaaaggccc atggggtcaa     600
caagtatggc acaaagcgtc gaacggagag tatttctacg caacgttctg ggaagggatg     660
ccggacttaa actatgacaa ccctaaagta agagaagaaa tgattaaaat cgggaaattt     720
tggctcaaac aaggagctga tggctttcgt ctagatgcag ccatgcacat ctttaaaggg     780
caaacacctg aaggagcaaa gaaaaatatt gaatggtgga atgaattccg cgacgcgatg     840
agagaaacga atccaaatac gtatctagtt ggtgaaatat gggatcaacc agaagtagtt     900
gctccgtatt atcaatcgtt agattctaca tttaacttcg acttagcata taaaatcgtt     960
aattccgtta aaaatggtac tgatcaaggg gtagccgcgg cagctgttgc aacggatgag    1020
ttatataaaa catataatcc aaataaaatt gatggaacgt ttttaacgaa tcatgaccaa    1080
aatcgtgtaa tgagtgagtt aaatggtgat gtaaacaaag caaaatcagc agcctctatt    1140
ctgttgacac tccctggtaa tccgttcatt tattatggcg aagaaatcgg catgacaggc    1200
```

caaaaaccag atgagttgat tcgtgagcct ttccgttggt atgaagatga taaagaaggt 1260
caaacgagct gggagactcc agtatataac attgatcata atggtgtttc agttgaagca 1320
caagataaac aaaaagcttc tcttctaagc cattatcgta aaatgattcg tgttcgtcag 1380
caacacgatg aacttgtcaa aggtaattta gaacctattt ctgtcaataa ttcacaggtt 1440
gttgcctata atcgtacgta taaaaataaa tcaattcaag tgtaccataa tatttcagac 1500
aagccggtta cattaactgt ttcaaacaaa ggaaaactga ttttttctag tgaattagga 1560
gcaaaaaagg aaaaatcaac attagtaatt ccagcgaata cgacagtgct agtaaagtaa 1620

<210> 154
<211> 539
<212> PRT
<213> Environmental

<400> 154
Met Pro Ser Ile Asn Ala Ser Asp Cys Lys Lys Lys Gly Asp Arg Ser
1 5 10 15
Met Lys Arg Lys Lys Trp Thr Ala Leu Ala Leu Ser Leu Pro Leu Val
20 25 30
Met Ser Leu Ser Thr Asn Ile Gln Ala Glu Thr Leu His Asn Asn Lys
35 40 45
Gly Gln Lys Ala Gln Thr Gly Asn Lys Asp Gly Ile Phe Tyr Glu Leu
50 55 60
Tyr Val Asn Ser Phe Tyr Asp Thr Asp Ser Asn Gly His Gly Asp Leu
65 70 75 80
Lys Gly Val Thr Lys Lys Leu Asp Tyr Leu Asn Asp Gly Asn Pro Arg
85 90 95
Thr Asn Asn Asp Leu Gln Ile Asn Gly Ile Trp Met Met Pro Ile Asn
100 105 110
Thr Ser Pro Ser Tyr His Lys Tyr Asp Val Thr Asp Tyr Tyr Asn Ile
115 120 125
Asp Pro Gln Tyr Gly Ser Leu Gln Asp Phe Arg Glu Leu Thr Thr Glu
130 135 140
Ala His Lys Arg Asn Val Lys Val Val Ile Asp Leu Val Ile Asn His
145 150 155 160
Thr Ser Ser Glu His Pro Trp Phe Val Asp Ala Leu Lys Asn Lys Asn
165 170 175
Ser Lys Tyr Arg Asp Tyr Tyr Ile Trp Ala Asp Lys Asn Thr Asp Leu
180 185 190
Asn Glu Lys Gly Pro Trp Gly Gln Gln Val Trp His Lys Ala Ser Asn
195 200 205
Gly Glu Tyr Phe Tyr Ala Thr Phe Trp Glu Gly Met Pro Asp Leu Asn
210 215 220
Tyr Asp Asn Pro Lys Val Arg Glu Glu Met Ile Lys Ile Gly Lys Phe
225 230 235 240
Trp Leu Lys Gln Gly Ala Asp Gly Phe Arg Leu Asp Ala Ala Met His
245 250 255
Ile Phe Lys Gly Gln Thr Pro Glu Gly Ala Lys Lys Asn Ile Glu Trp
260 265 270
Trp Asn Glu Phe Arg Asp Ala Met Arg Glu Thr Asn Pro Asn Thr Tyr
275 280 285
Leu Val Gly Glu Ile Trp Asp Gln Pro Glu Val Val Ala Pro Tyr Tyr
290 295 300
Gln Ser Leu Asp Ser Thr Phe Asn Phe Asp Leu Ala Tyr Lys Ile Val
305 310 315 320
Asn Ser Val Lys Asn Gly Thr Asp Gln Gly Val Ala Ala Ala Ala Val
325 330 335
Ala Thr Asp Glu Leu Tyr Lys Thr Tyr Asn Pro Asn Lys Ile Asp Gly

```
            340                 345                 350
Thr Phe Leu Thr Asn His Asp Gln Asn Arg Val Met Ser Glu Leu Asn
        355                 360                 365
Gly Asp Val Asn Lys Ala Lys Ser Ala Ala Ser Ile Leu Leu Thr Leu
    370                 375                 380
Pro Gly Asn Pro Phe Ile Tyr Tyr Gly Glu Glu Ile Gly Met Thr Gly
385                 390                 395                 400
Gln Lys Pro Asp Glu Leu Ile Arg Glu Pro Phe Arg Trp Tyr Glu Asp
                405                 410                 415
Asp Lys Glu Gly Gln Thr Ser Trp Glu Thr Pro Val Tyr Asn Ile Asp
            420                 425                 430
His Asn Gly Val Ser Val Glu Ala Gln Asp Lys Gln Lys Ala Ser Leu
        435                 440                 445
Leu Ser His Tyr Arg Lys Met Ile Arg Val Arg Gln Gln His Asp Glu
    450                 455                 460
Leu Val Lys Gly Asn Leu Glu Pro Ile Ser Val Asn Asn Ser Gln Val
465                 470                 475                 480
Val Ala Tyr Asn Arg Thr Tyr Lys Asn Lys Ser Ile Gln Val Tyr His
                485                 490                 495
Asn Ile Ser Asp Lys Pro Val Thr Leu Thr Val Ser Asn Lys Gly Lys
            500                 505                 510
Leu Ile Phe Ser Ser Glu Leu Gly Ala Lys Lys Glu Lys Ser Thr Leu
        515                 520                 525
Val Ile Pro Ala Asn Thr Thr Val Leu Val Lys
    530                 535
```

<210> 155
<211> 1773
<212> DNA
<213> Environmental

<400> 155

```
gtgtcaagaa tgtttgcaaa acgattcaaa acctctttac tgccgttatt cgctggattt      60
ttattgctgt ttcatttggt tctggcagga ccaacggctg cgaatgctga aacggctaac     120
aaatcaaatg agcttacagc accgtcgatc aaaagcggaa ccattcttca tgcttggaat     180
tggtcgttca atacgttaaa acacaatatg aaggatattc atgatgcagg atatacagcg     240
attcagacgt ctccgattaa ccaagtcaag gaagggaacc aaggaaataa aaacatgtcg     300
aactggtact ggctctatca gccgacatcg taccaaattg gcaaccgtta cttaggtact     360
gaacaagaat ttaaagaaat gtgtgcagcc gctgaagaat atggcataaa ggttattgtt     420
gacgcggtca tcaatcatac caccagtgac tatgccgcga tttccaatga gattaagagt     480
attccaaact ggacacatgg aaacacacaa attaaaaact ggtctgatcg atgggatgtc     540
acgcagaatg cattgctcgg gctgtatgac tggaatacac aaaatacaca agtacagtcc     600
tatttgaaac ggttcttaga aagagcattg aatgacgggg cagacggttt tcgatttgat     660
gccgccaaac atatagagct tccggatgat ggcagttacg gcagtcaatt ttggccgaat     720
atcacaaata catctgcaga gttccaatac ggagaaatcc tgcaggatag tgcttcaaga     780
gatgcttcat atgcgaatta tatgaatgtg acagcgtcta actatgggca ttccataagg     840
tccgctttaa agaatcgtaa tctgggcgtg tcgaatatct cccactatgc atcagatgtg     900
tctgcggaca agctagtgac atgggtagaa tcgcatgata cgtatgccaa tgatgatgaa     960
gagtcgacat ggatgagcga tgatgatatc cgtttaggct gggcggtgat agcttctcgt    1020
tcaggcagta cgcctctttt cttttccaga cctgagggag gcggaaatgg tgtgagattc    1080
ccggggaaaa gccaaatagg cgatcgcggg agtgctttat ttgaagatca ggctatcact    1140
gcggtcaata gatttcacaa tgtgatggct ggacagcctg aggaactctc gaacccaaat    1200
ggaaacaacc agatatttat gaatcagcgc ggctcacatg gcgttgtgct ggcaaatgca    1260
ggttcatcct ctgtttctat caatacgcca acaaaattgc ctgatggcag gtatgataat    1320
aaagctgggg caggttcatt tcaagtaaat gacggtaaac tgacaggcac gatcaatgcc    1380
aggtctgtgg ctgtgcttta tcctgatgat attgcaaaag cgcctcatgt tttccttgag    1440
aattacaaaa caggtgtaac acattctttc aatgatcaac tgacgattac actgcgtgca    1500
```

```
gatgcgaata caacaaaagc cgtttatcaa atcaataatg gaccagagac ggcgtttaag    1560
gatggagatc aattcacaat cggaaaagga gatccatttg gcaaaacata caccatcatg    1620
ttaaaaggaa cgaacagtga tggtgtaacg aggaccgagg aatacagttt tgttaaaaga    1680
gatccagctt cggccaaaac catcggctat caaaatccga atcattggag ccaggtaaat    1740
gcttatatct ataaacatga tgggggccgg gca                                 1773
```

<210> 156
<211> 591
<212> PRT
<213> Environmental

<400> 156

```
Val Ser Arg Met Phe Ala Lys Arg Phe Lys Thr Ser Leu Leu Pro Leu
 1               5                  10                  15
Phe Ala Gly Phe Leu Leu Leu Phe His Leu Val Leu Ala Gly Pro Thr
            20                  25                  30
Ala Ala Asn Ala Glu Thr Ala Asn Lys Ser Asn Glu Leu Thr Ala Pro
        35                  40                  45
Ser Ile Lys Ser Gly Thr Ile Leu His Ala Trp Asn Trp Ser Phe Asn
    50                  55                  60
Thr Leu Lys His Asn Met Lys Asp Ile His Asp Ala Gly Tyr Thr Ala
65                  70                  75                  80
Ile Gln Thr Ser Pro Ile Asn Gln Val Lys Glu Gly Asn Gln Gly Asn
                85                  90                  95
Lys Asn Met Ser Asn Trp Tyr Trp Leu Tyr Gln Pro Thr Ser Tyr Gln
            100                 105                 110
Ile Gly Asn Arg Tyr Leu Gly Thr Glu Gln Glu Phe Lys Glu Met Cys
        115                 120                 125
Ala Ala Ala Glu Glu Tyr Gly Ile Lys Val Ile Val Asp Ala Val Ile
    130                 135                 140
Asn His Thr Thr Ser Asp Tyr Ala Ala Ile Ser Asn Glu Ile Lys Ser
145                 150                 155                 160
Ile Pro Asn Trp Thr His Gly Asn Thr Gln Ile Lys Asn Trp Ser Asp
                165                 170                 175
Arg Trp Asp Val Thr Gln Asn Ala Leu Leu Gly Leu Tyr Asp Trp Asn
            180                 185                 190
Thr Gln Asn Thr Gln Val Gln Ser Tyr Leu Lys Arg Phe Leu Glu Arg
        195                 200                 205
Ala Leu Asn Asp Gly Ala Asp Gly Phe Arg Phe Asp Ala Ala Lys His
    210                 215                 220
Ile Glu Leu Pro Asp Asp Gly Ser Tyr Gly Ser Gln Phe Trp Pro Asn
225                 230                 235                 240
Ile Thr Asn Thr Ser Ala Glu Phe Gln Tyr Gly Glu Ile Leu Gln Asp
                245                 250                 255
Ser Ala Ser Arg Asp Ala Ser Tyr Ala Asn Tyr Met Asn Val Thr Ala
            260                 265                 270
Ser Asn Tyr Gly His Ser Ile Arg Ser Ala Leu Lys Asn Arg Asn Leu
        275                 280                 285
Gly Val Ser Asn Ile Ser His Tyr Ala Ser Asp Val Ser Ala Asp Lys
    290                 295                 300
Leu Val Thr Trp Val Glu Ser His Asp Thr Tyr Ala Asn Asp Asp Glu
305                 310                 315                 320
Glu Ser Thr Trp Met Ser Asp Asp Asp Ile Arg Leu Gly Trp Ala Val
                325                 330                 335
Ile Ala Ser Arg Ser Gly Ser Thr Pro Leu Phe Phe Ser Arg Pro Glu
            340                 345                 350
Gly Gly Gly Asn Gly Val Arg Phe Pro Gly Lys Ser Gln Ile Gly Asp
```

```
        355                 360                 365
Arg Gly Ser Ala Leu Phe Glu Asp Gln Ala Ile Thr Ala Val Asn Arg
    370                 375                 380
Phe His Asn Val Met Ala Gly Gln Pro Glu Glu Leu Ser Asn Pro Asn
385                 390                 395                 400
Gly Asn Asn Gln Ile Phe Met Asn Gln Arg Gly Ser His Gly Val Val
                405                 410                 415
Leu Ala Asn Ala Gly Ser Ser Ser Val Ser Ile Asn Thr Pro Thr Lys
            420                 425                 430
Leu Pro Asp Gly Arg Tyr Asp Asn Lys Ala Gly Ala Gly Ser Phe Gln
        435                 440                 445
Val Asn Asp Gly Lys Leu Thr Gly Thr Ile Asn Ala Arg Ser Val Ala
    450                 455                 460
Val Leu Tyr Pro Asp Asp Ile Ala Lys Ala Pro His Val Phe Leu Glu
465                 470                 475                 480
Asn Tyr Lys Thr Gly Val Thr His Ser Phe Asn Asp Gln Leu Thr Ile
                485                 490                 495
Thr Leu Arg Ala Asp Ala Asn Thr Thr Lys Ala Val Tyr Gln Ile Asn
            500                 505                 510
Asn Gly Pro Glu Thr Ala Phe Lys Asp Gly Asp Gln Phe Thr Ile Gly
        515                 520                 525
Lys Gly Asp Pro Phe Gly Lys Thr Tyr Thr Ile Met Leu Lys Gly Thr
    530                 535                 540
Asn Ser Asp Gly Val Thr Arg Thr Glu Glu Tyr Ser Phe Val Lys Arg
545                 550                 555                 560
Asp Pro Ala Ser Ala Lys Thr Ile Gly Tyr Gln Asn Pro Asn His Trp
                565                 570                 575
Ser Gln Val Asn Ala Tyr Ile Tyr Lys His Asp Gly Gly Arg Ala
            580                 585                 590
```

<210> 157
<211> 1596
<212> DNA
<213> Environmental

<400> 157

```
atgcaaacga ttgcaaaaaa aggggatgaa acgatgaaag ggaaaaaatg gacagcatta      60
gctctaacac tgccgctggc tgctagctta tcaacaggcg ttcacgccga aaccgtacat     120
aaaggtaaag ctccaacagc agataaaaac ggtgtctttt atgaggtgta tgtaaactct     180
ttttacgatg caaataaaga tggacatggt gatttaaaag gtcttacaca aaagctggat     240
tatttgaatg acggcaattc tcataccaaa aatgatcttc aagtaaacgg aatttggatg     300
atgccggtaa acccttctcc tagctatcat aaatatgatg taacggacta ttataacatt     360
gatccgcagt acggaaatct gcaagatttt cgcaagctga tgaaagaagc agataaacga     420
gacgtaaagg ttattatgga cctcgttgtg aatcatacaa gcagtgaaca tccttggttt     480
caagctgcat taaaagataa aaacagcaag tacagagatt actatatttg ggccgataaa     540
aatactgatt taaatgaaaa aggatcttgg gggcagcaag tatggcataa agctccaaac     600
ggagagtatt tttatggtac gttttgggaa ggaatgcctg acttaaatta cgataatccc     660
gaagtaagaa aagaaatgat taacgtcggg aaattttggc taaagcaagg cgttgacggg     720
ttccgcttag atgctgcgct tcatattttt aaaggtcaaa cacctgaagg cgctaagaaa     780
aatatcgtgt ggtggaatga gtttagagat gcaatgaaaa aagaaaaccc taacgtatat     840
ctaacgggtg aagtatggga tcaaccggaa gtagtagctc cttactatca atcgcttgat     900
tctttattta actttgattt agcaggaaag attgtaaact ctgtaaaatc aggaaatgat     960
caaggaatcg cgactgcagc agccgcaact gatgagctgt tcaaatcata caatccaaat    1020
aaaattgacg gcattttctt aaccaaccat gaccaaaatc gcgtcatgag tgagctaagc    1080
ggcgatgtga ataaagcaaa gtcagctgcc tctatcttac ttacgcttcc tggcaacccg    1140
tatatttatt acggtgaaga aattggaatg accggtgaaa agcctgatga gttaatccgt    1200
gaaccgttcc gctggtacga aggcaatgga cttggacaaa ccagctggga aacatccgta    1260
```

```
tacaacaaag gcggcaatgg tgtgtcagta gagacacaaa caaaacaaaa ggattctttg    1320
ttaaatcatt accgtgaaat gattcgcgtg cgtcagcagc atgaagagtt agtaaaagga    1380
acccttcaat ctatttcagt agacagtaaa gaagtcgttg cctatagccg cacgtataaa    1440
ggcaaatcga ttagcgtgta tcataatatt tcaaatcaac cggtaaaagt atctgtaaca    1500
gcgaaaggta aattgatttt tgctagtgaa aaaggtgcaa aaaaagtcaa aaatcagctt    1560
gtggttccag ctaatacaac ggttttaata aaataa                              1596
```

<210> 158
<211> 531
<212> PRT
<213> Environmental

<400> 158

```
Met Gln Thr Ile Ala Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys
 1               5                  10                  15
Trp Thr Ala Leu Ala Leu Thr Leu Pro Leu Ala Ala Ser Leu Ser Thr
            20                  25                  30
Gly Val His Ala Glu Thr Val His Lys Gly Lys Ala Pro Thr Ala Asp
        35                  40                  45
Lys Asn Gly Val Phe Tyr Glu Val Tyr Val Asn Ser Phe Tyr Asp Ala
    50                  55                  60
Asn Lys Asp Gly His Gly Asp Leu Lys Gly Leu Thr Gln Lys Leu Asp
65                  70                  75                  80
Tyr Leu Asn Asp Gly Asn Ser His Thr Lys Asn Asp Leu Gln Val Asn
                85                  90                  95
Gly Ile Trp Met Met Pro Val Asn Pro Ser Pro Ser Tyr His Lys Tyr
            100                 105                 110
Asp Val Thr Asp Tyr Tyr Asn Ile Asp Pro Gln Tyr Gly Asn Leu Gln
        115                 120                 125
Asp Phe Arg Lys Leu Met Lys Glu Ala Asp Lys Arg Asp Val Lys Val
    130                 135                 140
Ile Met Asp Leu Val Val Asn His Thr Ser Ser Glu His Pro Trp Phe
145                 150                 155                 160
Gln Ala Ala Leu Lys Asp Lys Asn Ser Lys Tyr Arg Asp Tyr Tyr Ile
                165                 170                 175
Trp Ala Asp Lys Asn Thr Asp Leu Asn Glu Lys Gly Ser Trp Gly Gln
            180                 185                 190
Gln Val Trp His Lys Ala Pro Asn Gly Glu Tyr Phe Tyr Gly Thr Phe
        195                 200                 205
Trp Glu Gly Met Pro Asp Leu Asn Tyr Asp Asn Pro Glu Val Arg Lys
    210                 215                 220
Glu Met Ile Asn Val Gly Lys Phe Trp Leu Lys Gln Gly Val Asp Gly
225                 230                 235                 240
Phe Arg Leu Asp Ala Ala Leu His Ile Phe Lys Gly Gln Thr Pro Glu
                245                 250                 255
Gly Ala Lys Lys Asn Ile Val Trp Trp Asn Glu Phe Arg Asp Ala Met
            260                 265                 270
Lys Lys Glu Asn Pro Asn Val Tyr Leu Thr Gly Glu Val Trp Asp Gln
        275                 280                 285
Pro Glu Val Val Ala Pro Tyr Tyr Gln Ser Leu Asp Ser Leu Phe Asn
    290                 295                 300
Phe Asp Leu Ala Gly Lys Ile Val Asn Ser Val Lys Ser Gly Asn Asp
305                 310                 315                 320
Gln Gly Ile Ala Thr Ala Ala Ala Ala Thr Asp Glu Leu Phe Lys Ser
                325                 330                 335
Tyr Asn Pro Asn Lys Ile Asp Gly Ile Phe Leu Thr Asn His Asp Gln
            340                 345                 350
```

```
Asn Arg Val Met Ser Glu Leu Ser Gly Asp Val Asn Lys Ala Lys Ser
        355                 360                 365
Ala Ala Ser Ile Leu Leu Thr Leu Pro Gly Asn Pro Tyr Ile Tyr Tyr
    370                 375                 380
Gly Glu Glu Ile Gly Met Thr Gly Glu Lys Pro Asp Glu Leu Ile Arg
385                 390                 395                 400
Glu Pro Phe Arg Trp Tyr Glu Gly Asn Gly Leu Gly Gln Thr Ser Trp
                405                 410                 415
Glu Thr Ser Val Tyr Asn Lys Gly Gly Asn Gly Val Ser Val Glu Thr
            420                 425                 430
Gln Thr Lys Gln Lys Asp Ser Leu Leu Asn His Tyr Arg Glu Met Ile
        435                 440                 445
Arg Val Arg Gln Gln His Glu Glu Leu Val Lys Gly Thr Leu Gln Ser
    450                 455                 460
Ile Ser Val Asp Ser Lys Glu Val Val Ala Tyr Ser Arg Thr Tyr Lys
465                 470                 475                 480
Gly Lys Ser Ile Ser Val Tyr His Asn Ile Ser Asn Gln Pro Val Lys
                485                 490                 495
Val Ser Val Thr Ala Lys Gly Lys Leu Ile Phe Ala Ser Glu Lys Gly
            500                 505                 510
Ala Lys Lys Val Lys Asn Gln Leu Val Val Pro Ala Asn Thr Thr Val
        515                 520                 525
Leu Ile Lys
    530
```

<210> 159
<211> 1587
<212> DNA
<213> Environmental

<400> 159

```
atgcaaaaaa aaggggatga aacgatgaaa gggaaaaaat ggacagcttt agctctaaca      60
ctgccgctgg ctgctagctt atcaacaggc gttcacgccg aaaccgtaca taaaggtaaa     120
tctccaacag cagataaaaa cggtgtattt tatgaggtgt atgtaaactc tttttacgat     180
gcaaataaag atggacatgg tgatttaaaa ggtcttacac aaaagttgga ttatttaaat     240
gatggcaatt ctcatacaaa gaatgatctt caagtaaacg ggatttggat gatgccggtc     300
aacccttctc ccagctatca taaatatgat gtaacggact attataatat tgatccgcag     360
tatggaaatc tgcaagattt tcgcaaactg atgaaagaag cagataaacg agatgtaaaa     420
gtcattatgg acctcgttgt gaatcatacg agcagtgaac acccttggtt tcaagctgca     480
ttaaaagata aaaacagcaa gtacagagat tactatatct gggctgataa aaataccgac     540
ttgaatgaaa aaggatcttg gggacagcaa gtatggcata aagctccaaa cggagagtat     600
ttttacggaa cgttttggga aggaatgccg gacttaaatt acgataatcc tgaagtaaga     660
aaagaaatga ttaacgtagg aaagttttgg ctaaagcaag gagttgatgg gttccgtcta     720
gatgctgcgc ttcatatttt taaaggccaa acacctgaag gcgctaagaa aaatctcctg     780
tggtggaatg aatttagaga tgcaatgaaa aaggaaaacc ctaacgtata tctaacgggt     840
gaagtatggg atcaaccgga agtagtagct ccttactatc aatcgcttga ttctttattt     900
aactttgatt tagcaggaaa gattgtaaac tctgtaaaat caggaaatga tcaaggaatc     960
gcgactgcag cagcggcaac ggatgaactg ttcaaatcat acaatccaaa taaaattgac    1020
ggtatttttct taaccaacca tgaccaaaat cgcgtcatga gtgagctaaa cggcgatgtg    1080
aataaagcaa agtcagctgc ctctatctta cttacgcttc ctggcaaccc gtatatttat    1140
tacggtgaag aaatcggcat gaccggtgaa aagcctgatg agttaatccg tgaaccgttc    1200
ccctggtacg aaggaaacgg acttggacaa accagctggg aaacacctgt atataacaaa    1260
ggcggcaacg gcgtgtctgt agaagcacaa acaaaacaaa aggactcttt gttaaatcat    1320
taccgtgaaa tgattcgcgt gcgtcagcag cacgaagagt tagtaaaagg aacgcttcaa    1380
tctatttcag tagacagtaa agaagtcgtt gcctatagcc gtacgtataa aggcaaatcg    1440
attagcgtgt atcataatat ttcaaatcaa ccggtaaaag tatctgtagc agcaaaaggt    1500
aaattgattt ttgctagtga aaaaggtgct aagaaagtca aaaatcagct tgtgattccg    1560
```

gcgaatacaa cggttttaat aaaataa 1587

<210> 160
<211> 528
<212> PRT
<213> Environmental

<400> 160
Met Gln Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys Trp Thr Ala
1 5 10 15
Leu Ala Leu Thr Leu Pro Leu Ala Ala Ser Leu Ser Thr Gly Val His
20 25 30
Ala Glu Thr Val His Lys Gly Lys Ser Pro Thr Ala Asp Lys Asn Gly
35 40 45
Val Phe Tyr Glu Val Tyr Val Asn Ser Phe Tyr Asp Ala Asn Lys Asp
50 55 60
Gly His Gly Asp Leu Lys Gly Leu Thr Gln Lys Leu Asp Tyr Leu Asn
65 70 75 80
Asp Gly Asn Ser His Thr Lys Asn Asp Leu Gln Val Asn Gly Ile Trp
85 90 95
Met Met Pro Val Asn Pro Ser Pro Ser Tyr His Lys Tyr Asp Val Thr
100 105 110
Asp Tyr Tyr Asn Ile Asp Pro Gln Tyr Gly Asn Leu Gln Asp Phe Arg
115 120 125
Lys Leu Met Lys Glu Ala Asp Lys Arg Asp Val Lys Val Ile Met Asp
130 135 140
Leu Val Val Asn His Thr Ser Ser Glu His Pro Trp Phe Gln Ala Ala
145 150 155 160
Leu Lys Asp Lys Asn Ser Lys Tyr Arg Asp Tyr Tyr Ile Trp Ala Asp
165 170 175
Lys Asn Thr Asp Leu Asn Glu Lys Gly Ser Trp Gly Gln Gln Val Trp
180 185 190
His Lys Ala Pro Asn Gly Glu Tyr Phe Tyr Gly Thr Phe Trp Glu Gly
195 200 205
Met Pro Asp Leu Asn Tyr Asp Asn Pro Glu Val Arg Lys Glu Met Ile
210 215 220
Asn Val Gly Lys Phe Trp Leu Lys Gln Gly Val Asp Gly Phe Arg Leu
225 230 235 240
Asp Ala Ala Leu His Ile Phe Lys Gly Gln Thr Pro Glu Gly Ala Lys
245 250 255
Lys Asn Leu Leu Trp Trp Asn Glu Phe Arg Asp Ala Met Lys Lys Glu
260 265 270
Asn Pro Asn Val Tyr Leu Thr Gly Glu Val Trp Asp Gln Pro Glu Val
275 280 285
Val Ala Pro Tyr Tyr Gln Ser Leu Asp Ser Leu Phe Asn Phe Asp Leu
290 295 300
Ala Gly Lys Ile Val Asn Ser Val Lys Ser Gly Asn Asp Gln Gly Ile
305 310 315 320
Ala Thr Ala Ala Ala Ala Thr Asp Glu Leu Phe Lys Ser Tyr Asn Pro
325 330 335
Asn Lys Ile Asp Gly Ile Phe Leu Thr Asn His Asp Gln Asn Arg Val
340 345 350
Met Ser Glu Leu Asn Gly Asp Val Asn Lys Ala Lys Ser Ala Ala Ser
355 360 365
Ile Leu Leu Thr Leu Pro Gly Asn Pro Tyr Ile Tyr Tyr Gly Glu Glu
370 375 380
Ile Gly Met Thr Gly Glu Lys Pro Asp Glu Leu Ile Arg Glu Pro Phe

```
385                 390                 395                 400
Pro Trp Tyr Glu Gly Asn Gly Leu Gly Gln Thr Ser Trp Glu Thr Pro
                405                 410                 415
Val Tyr Asn Lys Gly Gly Asn Gly Val Ser Val Glu Ala Gln Thr Lys
            420                 425                 430
Gln Lys Asp Ser Leu Leu Asn His Tyr Arg Glu Met Ile Arg Val Arg
        435                 440                 445
Gln Gln His Glu Glu Leu Val Lys Gly Thr Leu Gln Ser Ile Ser Val
    450                 455                 460
Asp Ser Lys Glu Val Val Ala Tyr Ser Arg Thr Tyr Lys Gly Lys Ser
465                 470                 475                 480
Ile Ser Val Tyr His Asn Ile Ser Asn Gln Pro Val Lys Val Ser Val
                485                 490                 495
Ala Ala Lys Gly Lys Leu Ile Phe Ala Ser Glu Lys Gly Ala Lys Lys
            500                 505                 510
Val Lys Asn Gln Leu Val Ile Pro Ala Asn Thr Thr Val Leu Ile Lys
        515                 520                 525
```

<210> 161
<211> 1623
<212> DNA
<213> Bacterial

<400> 161

```
gtggatccaa agaattgtag tcaatttatg caaacgattg caaaaaaagg ggatgaaacg      60
atgaaaggga aaaaatggac agctttagct ctaacactgc cgctggctgc tagcttatca     120
acaggtgttc acgccgaaac cgtacataaa ggtaaagctc caacagcaga taaaaacggt     180
gtcttttatg aggtatatgt aaactctttt tacgatgcaa ataaagatgg acatggtgat     240
ttaaaaggcc ttacacaaaa gttggactat ttaaatgacg gaaattctca tacaaagaat     300
gatcttcaag taaacgggat ttggatgatg ccggtcaacc cttctcctag ctatcataaa     360
tatgatgtaa cggactatta taatattgat ccgcagtatg gaaatctgca agattttcgc     420
aaacttatga aagaagcaga taaacgagac gtaaaagtca ttatggacct tgttgtgaat     480
catacgagca gtgaacaccc ttggtttcaa gctgcgttga aagataaaaa cagcaagtac     540
agagattact atatttgggc tgataaaaat actgacttga atgaaaaagg atcttgggga     600
caacaagtat ggcataaagc tccaaacgga gagtattttt acggaacgtt ctgggaagga     660
atgcctgact taaattacga taaccctgaa gtaagaaaag aaatgattaa cgtcggaaag     720
ttttggctaa aacaaggcgt tgacggcttc cgcttagatg ctgcccttca tatttttaaa     780
ggtcaaacgc ctgaaggcgc taagaaaaac attctatggt ggaatgagtt tagagatgcg     840
atgaaaaaag aaaacccgaa cgtatatcta acgggtgaag tgtgggacca gccagaagta     900
gtagcccctt actatcaatc acttgattct ctatttaatt ttgatttagc aggaaaaatt     960
gtcagctctg taaaagcagg aaatgatcaa ggaatcgcca ctgcagcagc ggcaactgat    1020
gagctgttca aatcatacaa tccaaataaa attgacggca ttttcttaac caaccatgac    1080
caaaatcgcg tcatgagtga gttaagcggc gatgtgaata aagcaaaatc agccgcctct    1140
atcttactta cgcttcctgg aaatccgtat atttattacg gtgaagaaat tggcatgaca    1200
ggtgaaaagc ctgatgaatt aatccgtgaa ccgttccgct ggtacgaagg caacggaatt    1260
ggacaaacta gctgggaaac acctgtatat aacaaaggcg gtaacggcgt gtctgtagaa    1320
gcacaaacaa aacaaaagga ttccttgtta aatcattacc gtgaaatgat tcgtgtgcgc    1380
cagcagcacg aagagttagt aaaaggaacg cttcaatcca tttcagtaga cagtaaagaa    1440
gtcgttgcct atagccgcac gtacaaaggc aaatcgatta gcgtgtatca taatatttca    1500
aatcaacctg taaaagtatc tgtagcagcg aaaggtaact tgatttttgc tagtgaaaaa    1560
ggtgctaaga aagtcaaaaa tcagcttgtg attccggcga atgcgacggt tttaataaaa    1620
taa                                                                 1623
```

<210> 162
<211> 540
<212> PRT
<213> Bacterial

<400> 162
Val Asp Pro Lys Asn Cys Ser Gln Phe Met Gln Thr Ile Ala Lys Lys
1 5 10 15
Gly Asp Glu Thr Met Lys Gly Lys Lys Trp Thr Ala Leu Ala Leu Thr
20 25 30
Leu Pro Leu Ala Ala Ser Leu Ser Thr Gly Val His Ala Glu Thr Val
35 40 45
His Lys Gly Lys Ala Pro Thr Ala Asp Lys Asn Gly Val Phe Tyr Glu
50 55 60
Val Tyr Val Asn Ser Phe Tyr Asp Ala Asn Lys Asp Gly His Gly Asp
65 70 75 80
Leu Lys Gly Leu Thr Gln Lys Leu Asp Tyr Leu Asn Asp Gly Asn Ser
85 90 95
His Thr Lys Asn Asp Leu Gln Val Asn Gly Ile Trp Met Met Pro Val
100 105 110
Asn Pro Ser Pro Ser Tyr His Lys Tyr Asp Val Thr Asp Tyr Tyr Asn
115 120 125
Ile Asp Pro Gln Tyr Gly Asn Leu Gln Asp Phe Arg Lys Leu Met Lys
130 135 140
Glu Ala Asp Lys Arg Asp Val Lys Val Ile Met Asp Leu Val Val Asn
145 150 155 160
His Thr Ser Ser Glu His Pro Trp Phe Gln Ala Ala Leu Lys Asp Lys
165 170 175
Asn Ser Lys Tyr Arg Asp Tyr Tyr Ile Trp Ala Asp Lys Asn Thr Asp
180 185 190
Leu Asn Glu Lys Gly Ser Trp Gly Gln Gln Val Trp His Lys Ala Pro
195 200 205
Asn Gly Glu Tyr Phe Tyr Gly Thr Phe Trp Glu Gly Met Pro Asp Leu
210 215 220
Asn Tyr Asp Asn Pro Glu Val Arg Lys Glu Met Ile Asn Val Gly Lys
225 230 235 240
Phe Trp Leu Lys Gln Gly Val Asp Gly Phe Arg Leu Asp Ala Ala Leu
245 250 255
His Ile Phe Lys Gly Gln Thr Pro Glu Gly Ala Lys Lys Asn Ile Leu
260 265 270
Trp Trp Asn Glu Phe Arg Asp Ala Met Lys Lys Glu Asn Pro Asn Val
275 280 285
Tyr Leu Thr Gly Glu Val Trp Asp Gln Pro Glu Val Val Ala Pro Tyr
290 295 300
Tyr Gln Ser Leu Asp Ser Leu Phe Asn Phe Asp Leu Ala Gly Lys Ile
305 310 315 320
Val Ser Ser Val Lys Ala Gly Asn Asp Gln Gly Ile Ala Thr Ala Ala
325 330 335
Ala Ala Thr Asp Glu Leu Phe Lys Ser Tyr Asn Pro Asn Lys Ile Asp
340 345 350
Gly Ile Phe Leu Thr Asn His Asp Gln Asn Arg Val Met Ser Glu Leu
355 360 365
Ser Gly Asp Val Asn Lys Ala Lys Ser Ala Ala Ser Ile Leu Leu Thr
370 375 380
Leu Pro Gly Asn Pro Tyr Ile Tyr Tyr Gly Glu Glu Ile Gly Met Thr
385 390 395 400
Gly Glu Lys Pro Asp Glu Leu Ile Arg Glu Pro Phe Arg Trp Tyr Glu
405 410 415
Gly Asn Gly Ile Gly Gln Thr Ser Trp Glu Thr Pro Val Tyr Asn Lys
420 425 430
Gly Gly Asn Gly Val Ser Val Glu Ala Gln Thr Lys Gln Lys Asp Ser

```
        435                 440                 445
Leu Leu Asn His Tyr Arg Glu Met Ile Arg Val Arg Gln Gln His Glu
    450                 455                 460
Glu Leu Val Lys Gly Thr Leu Gln Ser Ile Ser Val Asp Ser Lys Glu
465                 470                 475                 480
Val Val Ala Tyr Ser Arg Thr Tyr Lys Gly Lys Ser Ile Ser Val Tyr
                485                 490                 495
His Asn Ile Ser Asn Gln Pro Val Lys Val Ser Val Ala Ala Lys Gly
            500                 505                 510
Asn Leu Ile Phe Ala Ser Glu Lys Gly Ala Lys Lys Val Lys Asn Gln
        515                 520                 525
Leu Val Ile Pro Ala Asn Ala Thr Val Leu Ile Lys
    530                 535                 540
```

<210> 163
<211> 1422
<212> DNA
<213> Environmental

<400> 163

```
atggtacgtc ccgaacgacg ggctgcattg gaaccgacta tcgaacgact cgcagcactt     60
gaaagacatt gggtgacgac ggtgtggatt ccgccggcgt acaaaggcac gtcacagaac    120
gatgtcgggt atggggcgta cgatttatac gatctcggcg aattcaacca aaaagggacg    180
acccggacga agtacgggac gaaagcgcag ctccagaccg ccatctcgaa cttgcgcggt    240
aaagggatcg gtgtgtacgg cgacgtcgtc atgaatcaca agggcggggc cgattatacc    300
gaatccgttc aggcgatcga ggtcaatccg tcgaaccgga accaagaaac gtccggtgag    360
tatggcatct cggcctggac tgggttcaac ttcgcggggc gcaacaatac atactcgccg    420
ttcaaatggc gctggtacca ttttgacggt accgattggg atcagtcacg cagcttgagc    480
cgcatctata agttcaagag cacaggcaag gcgtgggaca cggacgtgtc gaacgagaac    540
ggcaactatg attatcttat gtatgccgac gtcgatttcg agcatcccga ggtccgccaa    600
gagatgaaga actggggcaa atggtacgcc gactcgctcg ggctcgacgg tttccggttg    660
gatgcggtca aacatatcag ccactcgtac ttgaaggagt gggtgacgag cgtgcgccag    720
acgaccggga aagagatgtt cacggtcgcc gagtattgga agaacgatct cggtgccatc    780
aacgactatc tgtataagac gggctacacg cactccgtct tcgatgtgcc gctccattat    840
aacttccaag cggccggtaa cggcggcggg tattacgata tgcgcaacat cttgaaaggc    900
accgtcaccg aacagcatcc gtcgctgtcc gtgacgattg tcgataacca cgactcacag    960
ccgggccagt cgctcgagtc gacggtcgcc aactggttca aaccgctcgc ctacgcgacg   1020
atcatgacgc gcggtcaggg ttatccggcc ctcttctatg gagactatta tggcacgaaa   1080
gggacgacga accgcgaaat cccgaacatg tcgggcacgc tccaaccgat tttgaaggca   1140
cgaaaagact tcgcctacgg gacgcagcat gactacctcg atcatcagga cgtcatcggc   1200
tggacacgtg aaggtgtgac cgaccgtgcc aaatcgggtc tcgcgacgat tctatcggac   1260
ggtccgggcg gctcgaagtg gatgtacgtc ggcaaacaga acgccggcga ggtatggaaa   1320
gacatgacga acaacaacgc ccgtctcgtc acgatcaatg ctgacggctg gggtcagttc   1380
ttcgtcaacg gaggctcggt ctcgatttat acgcaacaat aa                      1422
```

<210> 164
<211> 473
<212> PRT
<213> Environmental

<400> 164

```
Met Val Arg Pro Glu Arg Arg Ala Ala Leu Glu Pro Thr Ile Glu Arg
 1               5                  10                  15
Leu Ala Ala Leu Glu Arg His Trp Val Thr Thr Val Trp Ile Pro Pro
            20                  25                  30
Ala Tyr Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp
        35                  40                  45
```

```
Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Thr Arg Thr Lys
    50                  55                  60
Tyr Gly Thr Lys Ala Gln Leu Gln Thr Ala Ile Ser Asn Leu Arg Gly
65                  70                  75                  80
Lys Gly Ile Gly Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly
                85                  90                  95
Ala Asp Tyr Thr Glu Ser Val Gln Ala Ile Glu Val Asn Pro Ser Asn
            100                 105                 110
Arg Asn Gln Glu Thr Ser Gly Glu Tyr Gly Ile Ser Ala Trp Thr Gly
        115                 120                 125
Phe Asn Phe Ala Gly Arg Asn Asn Thr Tyr Ser Pro Phe Lys Trp Arg
    130                 135                 140
Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Ser Leu Ser
145                 150                 155                 160
Arg Ile Tyr Lys Phe Lys Ser Thr Gly Lys Ala Trp Asp Thr Asp Val
                165                 170                 175
Ser Asn Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp
            180                 185                 190
Phe Glu His Pro Glu Val Arg Gln Glu Met Lys Asn Trp Gly Lys Trp
        195                 200                 205
Tyr Ala Asp Ser Leu Gly Leu Asp Gly Phe Arg Leu Asp Ala Val Lys
    210                 215                 220
His Ile Ser His Ser Tyr Leu Lys Glu Trp Val Thr Ser Val Arg Gln
225                 230                 235                 240
Thr Thr Gly Lys Glu Met Phe Thr Val Ala Glu Tyr Trp Lys Asn Asp
                245                 250                 255
Leu Gly Ala Ile Asn Asp Tyr Leu Tyr Lys Thr Gly Tyr Thr His Ser
            260                 265                 270
Val Phe Asp Val Pro Leu His Tyr Asn Phe Gln Ala Ala Gly Asn Gly
        275                 280                 285
Gly Gly Tyr Tyr Asp Met Arg Asn Ile Leu Lys Gly Thr Val Thr Glu
    290                 295                 300
Gln His Pro Ser Leu Ser Val Thr Ile Val Asp Asn His Asp Ser Gln
305                 310                 315                 320
Pro Gly Gln Ser Leu Glu Ser Thr Val Ala Asn Trp Phe Lys Pro Leu
                325                 330                 335
Ala Tyr Ala Thr Ile Met Thr Arg Gly Gln Gly Tyr Pro Ala Leu Phe
            340                 345                 350
Tyr Gly Asp Tyr Tyr Gly Thr Lys Gly Thr Thr Asn Arg Glu Ile Pro
        355                 360                 365
Asn Met Ser Gly Thr Leu Gln Pro Ile Leu Lys Ala Arg Lys Asp Phe
    370                 375                 380
Ala Tyr Gly Thr Gln His Asp Tyr Leu Asp His Gln Asp Val Ile Gly
385                 390                 395                 400
Trp Thr Arg Glu Gly Val Thr Asp Arg Ala Lys Ser Gly Leu Ala Thr
                405                 410                 415
Ile Leu Ser Asp Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Lys
            420                 425                 430
Gln Asn Ala Gly Glu Val Trp Lys Asp Met Thr Asn Asn Asn Ala Arg
        435                 440                 445
Leu Val Thr Ile Asn Ala Asp Gly Trp Gly Gln Phe Phe Val Asn Gly
    450                 455                 460
Gly Ser Val Ser Ile Tyr Thr Gln Gln
465                 470
```

<210> 165
<211> 1437

<212> DNA
<213> Bacterial

<400> 165
atgcagtatt tcgagtggta cgtgccaaat gatggggaac attggaatcg tttgcgtaat 60
gatgctgaaa atttagctca taaaggaatt acatctgtat ggataccacc cgtatataaa 120
ggaacttcac aaaatgatgt agggtatgga gtgtatgatg tatatgattt gggagaattc 180
aatcaaaaag gaacgatacg gacaaaatat gggacaaaag cacaattaaa atctgcaatt 240
gaggctttac ataatcaaaa tatcgatgta tacggtgatg ttgttatgaa ccataaaggt 300
ggggcagatt atactgaggt tgtaacagcc gttgaggtag accgtaacaa tcgaaatatt 360
gaaacatcga gtgattatca aatagatgcg tggacgggat ttgattttcc aggacgcagg 420
gactcctatt ctaattttaa atggagatgg tttcattttg atggaacaga ttgggatgag 480
ggaaggaaat taaatagaat ttataaattt aaaggcgtag gtaaagcttg ggactgggaa 540
gtgtctagtg agaatggtaa ctatgattat ttaatgtatg cagatcttga tttcgatcat 600
cctgaagttg caaatgaaat gaaaaactgg ggaacctggt atgcggacga attaaattta 660
gatggctttc gtttagacgc agttaaacat attgaccatg agtatcttcg tgattgggta 720
aatcatgtta gaaagcaaac ggggaaggaa atgtttacag tagctgaata ttggcaaaat 780
gatattcgta ctttaaacaa ttatttaggg aaagtaaatt ataatcaatc tgtgttcgat 840
gcacctcttc attataattt tcattatgct tcaacaggga atggaaatta tgatatgagg 900
aatattttaa agggtacggt agtagaaagt catcctacac ttgctgttac tcttgttgag 960
aatcatgatt ctcagcctgg acagtcatta gaatctgttg tgagtccttg gtttaagccg 1020
ttggcctatg catttatttt aacgcgtgca gaagggtatc cttctgtttt ttatggagat 1080
tactatggca caaatggaaa tagtagttat gaaattccaa cgttaaagga taaaattgat 1140
ccaattctga cggcacgaaa aaactttgca tatggtacgc aacatgatta tttagaccat 1200
ccagatgtga ttggctggac aagagaaggg gatagtatac atgctaattc tggtttagca 1260
acattaatct ctgatggacc aggaggatca aaatggatga atgttggaaa gaacaacgca 1320
ggggaaatat ggtacgatat tacgggcaat caaacaaata ctgtaacgat taataaagat 1380
ggatgggggc agttccatgt aaatgggggc tctgtttcaa tatatgttca gaagtaa 1437

<210> 166
<211> 478
<212> PRT
<213> Bacterial

<400> 166
Met Gln Tyr Phe Glu Trp Tyr Val Pro Asn Asp Gly Glu His Trp Asn
1 5 10 15
Arg Leu Arg Asn Asp Ala Glu Asn Leu Ala His Lys Gly Ile Thr Ser
20 25 30
Val Trp Ile Pro Pro Val Tyr Lys Gly Thr Ser Gln Asn Asp Val Gly
35 40 45
Tyr Gly Val Tyr Asp Val Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly
50 55 60
Thr Ile Arg Thr Lys Tyr Gly Thr Lys Ala Gln Leu Lys Ser Ala Ile
65 70 75 80
Glu Ala Leu His Asn Gln Asn Ile Asp Val Tyr Gly Asp Val Val Met
85 90 95
Asn His Lys Gly Gly Ala Asp Tyr Thr Glu Val Val Thr Ala Val Glu
100 105 110
Val Asp Arg Asn Asn Arg Asn Ile Glu Thr Ser Ser Asp Tyr Gln Ile
115 120 125
Asp Ala Trp Thr Gly Phe Asp Phe Pro Gly Arg Arg Asp Ser Tyr Ser
130 135 140
Asn Phe Lys Trp Arg Trp Phe His Phe Asp Gly Thr Asp Trp Asp Glu
145 150 155 160
Gly Arg Lys Leu Asn Arg Ile Tyr Lys Phe Lys Gly Val Gly Lys Ala
165 170 175

```
Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met
            180                 185                 190
Tyr Ala Asp Leu Asp Phe Asp His Pro Glu Val Ala Asn Glu Met Lys
        195                 200                 205
Asn Trp Gly Thr Trp Tyr Ala Asp Glu Leu Asn Leu Asp Gly Phe Arg
    210                 215                 220
Leu Asp Ala Val Lys His Ile Asp His Glu Tyr Leu Arg Asp Trp Val
225                 230                 235                 240
Asn His Val Arg Lys Gln Thr Gly Lys Glu Met Phe Thr Val Ala Glu
                245                 250                 255
Tyr Trp Gln Asn Asp Ile Arg Thr Leu Asn Asn Tyr Leu Gly Lys Val
            260                 265                 270
Asn Tyr Asn Gln Ser Val Phe Asp Ala Pro Leu His Tyr Asn Phe His
        275                 280                 285
Tyr Ala Ser Thr Gly Asn Gly Asn Tyr Asp Met Arg Asn Ile Leu Lys
    290                 295                 300
Gly Thr Val Val Glu Ser His Pro Thr Leu Ala Val Thr Leu Val Glu
305                 310                 315                 320
Asn His Asp Ser Gln Pro Gly Gln Ser Leu Glu Ser Val Val Ser Pro
                325                 330                 335
Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Ala Glu Gly
            340                 345                 350
Tyr Pro Ser Val Phe Tyr Gly Asp Tyr Tyr Gly Thr Asn Gly Asn Ser
        355                 360                 365
Ser Tyr Glu Ile Pro Thr Leu Lys Asp Lys Ile Asp Pro Ile Leu Thr
    370                 375                 380
Ala Arg Lys Asn Phe Ala Tyr Gly Thr Gln His Asp Tyr Leu Asp His
385                 390                 395                 400
Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Ser Ile His Ala Asn
                405                 410                 415
Ser Gly Leu Ala Thr Leu Ile Ser Asp Gly Pro Gly Gly Ser Lys Trp
            420                 425                 430
Met Asn Val Gly Lys Asn Asn Ala Gly Glu Ile Trp Tyr Asp Ile Thr
        435                 440                 445
Gly Asn Gln Thr Asn Thr Val Thr Ile Asn Lys Asp Gly Trp Gly Gln
    450                 455                 460
Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln Lys
465                 470                 475
```

<210> 167
<211> 1596
<212> DNA
<213> Environmental

<400> 167

```
atgcaaacga ttgcaaaaaa aggggatgaa acgatgaaag ggaaaaaatg gacagcttta      60
gctctaacac tgccgctggc tgctagctta tcaacaggcg ttcacgccga aaccgtacat     120
aaaggtaaat ctccaacagc agataaaaac ggtgtatttt atgaggtgta tgtaaactct     180
ttttacgatg caaataaaga tggacatggt gatttaaaag gtcttacaca aaagttggat     240
tatttaaatg atggcaattc tcatacaaag aatgatcttc aagtaaacgg gatttggatg     300
atgccggtca acccttctcc cagctatcat aaatatgatg taacggacta ttataatatt     360
gatccgcagt atggaaatct gcaagatttt cgcaaactga tgaaagaagc agataaacga     420
gatgtaaaag tcattatgga cctcgttgtg aatcatacga gcagtgaaca cccttggttt     480
caagctgcat taaaagataa aaacagcaag tacagagatt actatatctg ggctgataaa     540
aataccgact tgaatgaaaa aggatcttgg ggacagcaag tatggcataa agccccaaac     600
ggagagtatt tttacggaac gttttgggaa ggaatgccgg acttaaatta cgataatcct     660
gaagtaagaa aagaaatgat taacgtagga aagttttggc taaagcaagg agttgacggg     720
```

```
ttccgtctag atgctgcgct tcatattttt aaaggccaaa cacctgaagg cgctaagaaa     780
aatctcctgt ggtggaatga atttagagat gcaatgaaaa aggaaaaccc taacgtatat     840
ctaacgggtg aagtatggga tcaaccggaa gtagtagctc cttactatca atcgcttgat     900
tctttattta actttgattt agcaggaaag attgtaaact ctgtaaaatc aggaaatgat     960
caaggaatcg cgactgcagc agcggcaacg gatgaactgt tcaaatcata caatccaaat    1020
aaaattgacg gtattttctt aaccaaccat gaccaaaatc gcgtcatgag tgagctaagc    1080
ggcgatgtga ataaagcaaa gtcagctgcc tctatcttac ttacgcttcc tggcaacccg    1140
tatatttatt acggtgaaga aatcggcatg accggtgaaa agcctgatga gttaatccgt    1200
gaaccgttcc gctggtacga aggaaacgga cttggacaaa ccagctggga aacacctgta    1260
tacaacaaag gcggcaacgg cgtgtctgta gaagcacaaa caaaacaaaa ggactctttg    1320
ttaaatcatt accgtgaaat gattcgcgtg cgtcagcagc acgaagagtt agtaaaagga    1380
acgcttcaat ctatttcagt agacagtaaa gaagtcgttg cctatagccg cacgtataaa    1440
ggcaaatcga ttagcgtgta tcataatatt tcaaatcaac cggtaaaagt atctgtagca    1500
gcaaaaggta aattgatttt tggtagtgaa aaaggtgcta agaaagtcaa aaatcagctt    1560
gtgattccgg cgaatacaac ggttttaata aaataa                              1596
```

<210> 168
<211> 531
<212> PRT
<213> Environmental

<400> 168

```
Met Gln Thr Ile Ala Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys
 1               5                  10                  15
Trp Thr Ala Leu Ala Leu Thr Leu Pro Leu Ala Ala Ser Leu Ser Thr
            20                  25                  30
Gly Val His Ala Glu Thr Val His Lys Gly Lys Ser Pro Thr Ala Asp
        35                  40                  45
Lys Asn Gly Val Phe Tyr Glu Val Tyr Val Asn Ser Phe Tyr Asp Ala
    50                  55                  60
Asn Lys Asp Gly His Gly Asp Leu Lys Gly Leu Thr Gln Lys Leu Asp
65                  70                  75                  80
Tyr Leu Asn Asp Gly Asn Ser His Thr Lys Asn Asp Leu Gln Val Asn
                85                  90                  95
Gly Ile Trp Met Met Pro Val Asn Pro Ser Pro Ser Tyr His Lys Tyr
            100                 105                 110
Asp Val Thr Asp Tyr Tyr Asn Ile Asp Pro Gln Tyr Gly Asn Leu Gln
        115                 120                 125
Asp Phe Arg Lys Leu Met Lys Glu Ala Asp Lys Arg Asp Val Lys Val
    130                 135                 140
Ile Met Asp Leu Val Val Asn His Thr Ser Ser Glu His Pro Trp Phe
145                 150                 155                 160
Gln Ala Ala Leu Lys Asp Lys Asn Ser Lys Tyr Arg Asp Tyr Tyr Ile
                165                 170                 175
Trp Ala Asp Lys Asn Thr Asp Leu Asn Glu Lys Gly Ser Trp Gly Gln
            180                 185                 190
Gln Val Trp His Lys Ala Pro Asn Gly Glu Tyr Phe Tyr Gly Thr Phe
        195                 200                 205
Trp Glu Gly Met Pro Asp Leu Asn Tyr Asp Asn Pro Glu Val Arg Lys
    210                 215                 220
Glu Met Ile Asn Val Gly Lys Phe Trp Leu Lys Gln Gly Val Asp Gly
225                 230                 235                 240
Phe Arg Leu Asp Ala Ala Leu His Ile Phe Lys Gly Gln Thr Pro Glu
                245                 250                 255
Gly Ala Lys Lys Asn Leu Leu Trp Trp Asn Glu Phe Arg Asp Ala Met
            260                 265                 270
Lys Lys Glu Asn Pro Asn Val Tyr Leu Thr Gly Glu Val Trp Asp Gln
```

```
        275                 280                 285
Pro Glu Val Val Ala Pro Tyr Tyr Gln Ser Leu Asp Ser Leu Phe Asn
    290                 295                 300
Phe Asp Leu Ala Gly Lys Ile Val Asn Ser Val Lys Ser Gly Asn Asp
305                 310                 315                 320
Gln Gly Ile Ala Thr Ala Ala Ala Ala Thr Asp Glu Leu Phe Lys Ser
                325                 330                 335
Tyr Asn Pro Asn Lys Ile Asp Gly Ile Phe Leu Thr Asn His Asp Gln
            340                 345                 350
Asn Arg Val Met Ser Glu Leu Ser Gly Asp Val Asn Lys Ala Lys Ser
        355                 360                 365
Ala Ala Ser Ile Leu Leu Thr Leu Pro Gly Asn Pro Tyr Ile Tyr Tyr
    370                 375                 380
Gly Glu Glu Ile Gly Met Thr Gly Glu Lys Pro Asp Glu Leu Ile Arg
385                 390                 395                 400
Glu Pro Phe Arg Trp Tyr Glu Gly Asn Gly Leu Gly Gln Thr Ser Trp
                405                 410                 415
Glu Thr Pro Val Tyr Asn Lys Gly Gly Asn Gly Val Ser Val Glu Ala
            420                 425                 430
Gln Thr Lys Gln Lys Asp Ser Leu Leu Asn His Tyr Arg Glu Met Ile
        435                 440                 445
Arg Val Arg Gln Gln His Glu Glu Leu Val Lys Gly Thr Leu Gln Ser
    450                 455                 460
Ile Ser Val Asp Ser Lys Glu Val Val Ala Tyr Ser Arg Thr Tyr Lys
465                 470                 475                 480
Gly Lys Ser Ile Ser Val Tyr His Asn Ile Ser Asn Gln Pro Val Lys
                485                 490                 495
Val Ser Val Ala Ala Lys Gly Lys Leu Ile Phe Gly Ser Glu Lys Gly
            500                 505                 510
Ala Lys Lys Val Lys Asn Gln Leu Val Ile Pro Ala Asn Thr Thr Val
        515                 520                 525
Leu Ile Lys
    530
```

<210> 169
<211> 1524
<212> DNA
<213> Environmental

<400> 169

```
atgaaaacat tcaaattaaa acgcactttt ttaccgctaa ccttgctgct cagtgctcct      60
gcctttgctg ggcaaaatgg caccatgatg cagtattttc attggtatgt acctaatgat     120
ggcgcattat ggacgcaggt tgaaagcaat gctccagcac tcgctgaaaa cggttttaca     180
gcgctctggc taccgccagc ttacaaaggc gcgggcggca gtaatgacgt cggttatggc     240
gtctatgata tgtacgattt aggtgagttt gatcaaaaag gctcagtacg aaccaaatac     300
ggcaccaagg ctcagtacat ctctgcaatc aatgccgcgc acaacaacaa tatccaaatc     360
tacggcgatg ttgtgtttaa ccaccgaggt ggtgctgatg ggaagtcgtg ggtcgatacc     420
aagcgcgttg attgggacaa ccgtaacatt gaactgggcg acaaatggat tgaagcttgg     480
gttgagttta attttcctgg ccgcaacgac aaatactcaa acttccattg gacttggtat     540
cactttgacg gtgttgactg ggatgatgcc ggcaaagaaa aagcgatctt taaattcaaa     600
ggcgaaggaa aagcatggga ttgggaagtc agctctgaaa aaggcaatta cgactaccta     660
atgtacgccg atttagacat ggatcaccaa gaagttaaac aagagctgaa agattggggt     720
gagtggtaca tcaacatgac cggcgttgat ggctttagaa tggatgccgt gaagcacatt     780
aaatatcagt atctacaaga gtggattgat catttacgtt ggaaaacagg caaagagctt     840
ttcaccgttg gtgagtattg gaattacgac gtaaatcaac tgcataactt tattactaag     900
acctctggca gtatgtcgtt gttcgatgcg ccgcttcaca tgaacttcta caacgcgtca     960
aaatctggcg gcaattacga tatgcgccaa atcatgaatg gcacgttgat gaaggacaac    1020
```

```
ccagtcaaag ctgtgactct cgtagaaaac cacgatacac agccattgca ggcgttagag    1080
tcgacagtgg attggtggtt caagcctctt gcttacgcat tcattttatt gcgtgaagaa    1140
ggttatccat cagtgttcta cgcagattac tacggcgcgc agtacagcga caaaggctac    1200
aacatcaata tggccaaagt tccttacatt gaagaacttg taacactgcg taaagagtat    1260
gcgtatggca aacagaattc ttatctcgac cactgggatg tgattggctg gacccgagag    1320
ggcgatgctg aacatccaaa ctcaatggcg gtgatcatga gtgatggacc aggtggcaaa    1380
aaatggatgt ataccggtaa gccaagcacg cgctatgtcg acaagctggg tatccgaact    1440
gaagaagttt ggaccgatac caatggctgg gcagaatttc ctgtcaatgg tggttcagtc    1500
tcggtttggg tgggcgttaa gtaa                                           1524

<210> 170
<211> 507
<212> PRT
<213> Environmental

<400> 170
Met Lys Thr Phe Lys Leu Lys Arg Thr Phe Leu Pro Leu Thr Leu Leu
 1               5                  10                  15
Leu Ser Ala Pro Ala Phe Ala Gly Gln Asn Gly Thr Met Met Gln Tyr
            20                  25                  30
Phe His Trp Tyr Val Pro Asn Asp Gly Ala Leu Trp Thr Gln Val Glu
        35                  40                  45
Ser Asn Ala Pro Ala Leu Ala Glu Asn Gly Phe Thr Ala Leu Trp Leu
    50                  55                  60
Pro Pro Ala Tyr Lys Gly Ala Gly Gly Ser Asn Asp Val Gly Tyr Gly
65                  70                  75                  80
Val Tyr Asp Met Tyr Asp Leu Gly Glu Phe Asp Gln Lys Gly Ser Val
                85                  90                  95
Arg Thr Lys Tyr Gly Thr Lys Ala Gln Tyr Ile Ser Ala Ile Asn Ala
            100                 105                 110
Ala His Asn Asn Asn Ile Gln Ile Tyr Gly Asp Val Val Phe Asn His
        115                 120                 125
Arg Gly Gly Ala Asp Gly Lys Ser Trp Val Asp Thr Lys Arg Val Asp
    130                 135                 140
Trp Asp Asn Arg Asn Ile Glu Leu Gly Asp Lys Trp Ile Glu Ala Trp
145                 150                 155                 160
Val Glu Phe Asn Phe Pro Gly Arg Asn Asp Lys Tyr Ser Asn Phe His
                165                 170                 175
Trp Thr Trp Tyr His Phe Asp Gly Val Asp Trp Asp Asp Ala Gly Lys
            180                 185                 190
Glu Lys Ala Ile Phe Lys Phe Lys Gly Glu Gly Lys Ala Trp Asp Trp
        195                 200                 205
Glu Val Ser Ser Glu Lys Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp
    210                 215                 220
Leu Asp Met Asp His Gln Glu Val Lys Gln Glu Leu Lys Asp Trp Gly
225                 230                 235                 240
Glu Trp Tyr Ile Asn Met Thr Gly Val Asp Gly Phe Arg Met Asp Ala
                245                 250                 255
Val Lys His Ile Lys Tyr Gln Tyr Leu Gln Glu Trp Ile Asp His Leu
            260                 265                 270
Arg Trp Lys Thr Gly Lys Glu Leu Phe Thr Val Gly Glu Tyr Trp Asn
        275                 280                 285
Tyr Asp Val Asn Gln Leu His Asn Phe Ile Thr Lys Thr Ser Gly Ser
    290                 295                 300
Met Ser Leu Phe Asp Ala Pro Leu His Met Asn Phe Tyr Asn Ala Ser
305                 310                 315                 320
Lys Ser Gly Gly Asn Tyr Asp Met Arg Gln Ile Met Asn Gly Thr Leu
```

```
                325                 330                 335
Met Lys Asp Asn Pro Val Lys Ala Val Thr Leu Val Glu Asn His Asp
            340                 345                 350
Thr Gln Pro Leu Gln Ala Leu Glu Ser Thr Val Asp Trp Trp Phe Lys
        355                 360                 365
Pro Leu Ala Tyr Ala Phe Ile Leu Leu Arg Glu Glu Gly Tyr Pro Ser
    370                 375                 380
Val Phe Tyr Ala Asp Tyr Tyr Gly Ala Gln Tyr Ser Asp Lys Gly Tyr
385                 390                 395                 400
Asn Ile Asn Met Ala Lys Val Pro Tyr Ile Glu Glu Leu Val Thr Leu
                405                 410                 415
Arg Lys Glu Tyr Ala Tyr Gly Lys Gln Asn Ser Tyr Leu Asp His Trp
            420                 425                 430
Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Ala Glu His Pro Asn Ser
        435                 440                 445
Met Ala Val Ile Met Ser Asp Gly Pro Gly Gly Lys Lys Trp Met Tyr
    450                 455                 460
Thr Gly Lys Pro Ser Thr Arg Tyr Val Asp Lys Leu Gly Ile Arg Thr
465                 470                 475                 480
Glu Glu Val Trp Thr Asp Thr Asn Gly Trp Ala Glu Phe Pro Val Asn
                485                 490                 495
Gly Gly Ser Val Ser Val Trp Val Gly Val Lys
            500                 505
```

<210> 171
<211> 1431
<212> DNA
<213> Environmental

<400> 171

```
gtgtatgtaa actcttttta cgatgcaaat aaagatggac atggtgattt aaaaggtctt      60
acacaaaagt tggattattt aaatgatggc aattctcata caaagaatga tcttcaagta     120
aacgggattt ggatgatgcc ggtcaaccct tctcccagct atcataaata tgatgtaacg     180
gactattata atattgatcc gcagtatgga aatctgcaag attttcgcaa actgatgaaa     240
gaagcagata aacgagatgt aaaagtcatt atggacctcg ttgtgaatca tacgagcagt     300
gaacaccctt ggtttcaagc tgcattaaaa gataaaaaca gcaagtacag agattactat     360
atctgggctg ataaaaatac cgacttgaat gaaaaaggat cttggggaca gcaagtatgg     420
cataaagccc caaacggaga gtatttttac ggaacgtttt gggaaggaat gccggactta     480
aattacgata atcctgaagt aagaaaagaa atgattaacg taggaaagtt ttggctaaag     540
caaggagttg acgggttccg tctagatgct gcgcttcata tttttaaagg ccaaacacct     600
gaaggcgcta agaaaaatct cctgtggtgg aatgaattta gagatgcaat gaaaaaggaa     660
aaccctaacg tatatctaac gggtgaagta tgggatcaac cggaagtagt agctccttac     720
tatcaatcgc ttgattcttt atttaacttt gatttagcag gaaagattgt aaactctgta     780
aaatcaggaa atgatcaagg aatcgcgact gcagcagcgg caacggatga actgttcaaa     840
tcatacaatc caaataaaat tgacggtatt ttcttaacca accatgacca aaatcgcgtc     900
atgagtgagc taagcggcga tgtgaataaa gcaaagtcag ctgcctctat cttacttacg     960
cttcctggca acccgtatat ttattacggt gaagaaatcg gcatgaccgg tgaaaagcct    1020
gatgagttaa tccgtgaacc gttccgctgg tacgaaggaa acggacttgg acaaaccagc    1080
tgggaaacac ctgtatacaa caaaggcggc aacggcgtgt ctgtagaagc acaaacaaaa    1140
caaaaggact ctttgttaaa tcattaccgt gaaatgattc gcgtgcgtca gcagcacgaa    1200
gagttagtaa aaggaacgct tcaatctatt tcagtagaca gtaaagaagt cgttgcctat    1260
agccgcacgt ataaaggcaa atcgattagc gtgtatcata atatttcaaa tcaaccggta    1320
aaagtatctg tagcagcaaa aggtaaattg atttttggta gtgaaaaagg tgctaagaaa    1380
gtcaaaaatc agcttgtgat tccggcgaat acaacggttt taataaaata a             1431
```

<210> 172
<211> 476

<212> PRT
<213> Environmental

<400> 172

```
Val Tyr Val Asn Ser Phe Tyr Asp Ala Asn Lys Asp Gly His Gly Asp
 1               5                  10                  15
Leu Lys Gly Leu Thr Gln Lys Leu Asp Tyr Leu Asn Asp Gly Asn Ser
            20                  25                  30
His Thr Lys Asn Asp Leu Gln Val Asn Gly Ile Trp Met Met Pro Val
        35                  40                  45
Asn Pro Ser Pro Ser Tyr His Lys Tyr Asp Val Thr Asp Tyr Tyr Asn
    50                  55                  60
Ile Asp Pro Gln Tyr Gly Asn Leu Gln Asp Phe Arg Lys Leu Met Lys
65                  70                  75                  80
Glu Ala Asp Lys Arg Asp Val Lys Val Ile Met Asp Leu Val Val Asn
                85                  90                  95
His Thr Ser Ser Glu His Pro Trp Phe Gln Ala Ala Leu Lys Asp Lys
            100                 105                 110
Asn Ser Lys Tyr Arg Asp Tyr Tyr Ile Trp Ala Asp Lys Asn Thr Asp
        115                 120                 125
Leu Asn Glu Lys Gly Ser Trp Gly Gln Gln Val Trp His Lys Ala Pro
    130                 135                 140
Asn Gly Glu Tyr Phe Tyr Gly Thr Phe Trp Glu Gly Met Pro Asp Leu
145                 150                 155                 160
Asn Tyr Asp Asn Pro Glu Val Arg Lys Glu Met Ile Asn Val Gly Lys
                165                 170                 175
Phe Trp Leu Lys Gln Gly Val Asp Gly Phe Arg Leu Asp Ala Ala Leu
            180                 185                 190
His Ile Phe Lys Gly Gln Thr Pro Glu Gly Ala Lys Lys Asn Leu Leu
        195                 200                 205
Trp Trp Asn Glu Phe Arg Asp Ala Met Lys Lys Glu Asn Pro Asn Val
    210                 215                 220
Tyr Leu Thr Gly Glu Val Trp Asp Gln Pro Glu Val Val Ala Pro Tyr
225                 230                 235                 240
Tyr Gln Ser Leu Asp Ser Leu Phe Asn Phe Asp Leu Ala Gly Lys Ile
                245                 250                 255
Val Asn Ser Val Lys Ser Gly Asn Asp Gln Gly Ile Ala Thr Ala Ala
            260                 265                 270
Ala Ala Thr Asp Glu Leu Phe Lys Ser Tyr Asn Pro Asn Lys Ile Asp
        275                 280                 285
Gly Ile Phe Leu Thr Asn His Asp Gln Asn Arg Val Met Ser Glu Leu
    290                 295                 300
Ser Gly Asp Val Asn Lys Ala Lys Ser Ala Ala Ser Ile Leu Leu Thr
305                 310                 315                 320
Leu Pro Gly Asn Pro Tyr Ile Tyr Tyr Gly Glu Glu Ile Gly Met Thr
                325                 330                 335
Gly Glu Lys Pro Asp Glu Leu Ile Arg Glu Pro Phe Arg Trp Tyr Glu
            340                 345                 350
Gly Asn Gly Leu Gly Gln Thr Ser Trp Glu Thr Pro Val Tyr Asn Lys
        355                 360                 365
Gly Gly Asn Gly Val Ser Val Glu Ala Gln Thr Lys Gln Lys Asp Ser
    370                 375                 380
Leu Leu Asn His Tyr Arg Glu Met Ile Arg Val Arg Gln Gln His Glu
385                 390                 395                 400
Glu Leu Val Lys Gly Thr Leu Gln Ser Ile Ser Val Asp Ser Lys Glu
                405                 410                 415
Val Val Ala Tyr Ser Arg Thr Tyr Lys Gly Lys Ser Ile Ser Val Tyr
```

```
            420                 425                 430
His Asn Ile Ser Asn Gln Pro Val Lys Val Ser Val Ala Ala Lys Gly
        435                 440                 445
Lys Leu Ile Phe Gly Ser Glu Lys Gly Ala Lys Lys Val Lys Asn Gln
    450                 455                 460
Leu Val Ile Pro Ala Asn Thr Thr Val Leu Ile Lys
465                 470                 475
```

<210> 173
<211> 1596
<212> DNA
<213> Environmental

<400> 173

```
atgcaaacga ttgcaaaaaa aggggatgaa acgatgaaag ggaaaaaatg gacagcttta      60
gctctaacac tgccgctggc tgctagctta tcaacaggcg ttcacgcaga aactgtacat     120
aaaggtaaag ctccaacagc agataaaaac ggtgtttttt atgaggtgta tgtaaactct     180
ttttacgatg caaataaaga tggacatggt gatttaaaag gtctgacaca aaagttggat     240
tatttaaatg acggcaattc tcatacaaag aatgatcttc aagtaaacgg gatttggatg     300
atgccggtaa acccttctcc tagctatcat aaatatgatg taacggacta ttataacatt     360
gatcctcagt acggaagtct gcaagatttc cgcaaactga tgaaagaagc agataaacga     420
gacgtaaaag ttattatgga ccttgttgtg aatcatacga gcagtgaaca cccttggttt     480
caagctgcac taaaagataa aaacagcaag tacagagatt actatatttg ggctgataaa     540
aataccgatt tgaatgaaaa aggatcttgg ggacagcaag tatggcataa agctccaaac     600
ggagagtatt tttacggaac gttctgggaa ggaatgcctg acttaaatta cgataaccct     660
gaagtaagaa aagaaatgat taacgtcgga aagttttggc taaagcaagg cgttgatggc     720
ttccgcttag atgctgccct tcatatcttt aaaggtcaaa ctcctgaagg cgctaagaaa     780
aatctcctgt ggtggaatga gtttagagat gcaatgaaaa aagaaaaccc taacgtatat     840
ctaacgggtg aagtatggga tcagccggaa gtagtagctc cttattatca atcgcttgat     900
tccctattta actttgattt agcaggaaaa attgtcagct ctgtaaaagc aggaaatgat     960
caaggaatcg ccactgcagc agcggcaacg gatgagctgt tcaaatcata caatccaaat    1020
aaaattgacg gcattttctt aaccaaccat gaccaaaacc gcgtcatgag tgagctaagc    1080
ggagatgtga ataaagcaaa atcagctgct tctatcttac ttacgcttcc tggaaatccg    1140
tatatttatt acggtgaaga aattggcatg accggtgaaa agcctgatga attaatccgt    1200
gaaccgttcc gctggtacga aggcaacgga attggacaaa ctagctggga aacacctgta    1260
tataacaaag gcggcaatgg tgtgtctgta gaagcacaaa ccaaacaaaa ggattctttg    1320
ttaaatcatt accgtgaaat gattcgcgtg cgtcagcagc acgaagagtt agtaaaagga    1380
acgcttcagt ctatttcagt agacagtaaa gaagttgtcg cttatagccg tacgtataaa    1440
ggcaactcca ttagtgtgta tcataatatt tcaaatcaac ctgtaaaagt atctgtagcg    1500
gcgaaaggta aattgatttt tgctagtgaa aaaggtgcta aaaaaggcaa aaatcagctt    1560
gtgattccgg cgaatgcgac ggttttaata aaataa                              1596
```

<210> 174
<211> 531
<212> PRT
<213> Environmental

<400> 174

```
Met Gln Thr Ile Ala Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys
 1               5                  10                  15
Trp Thr Ala Leu Ala Leu Thr Leu Pro Leu Ala Ala Ser Leu Ser Thr
            20                  25                  30
Gly Val His Ala Glu Thr Val His Lys Gly Lys Ala Pro Thr Ala Asp
        35                  40                  45
Lys Asn Gly Val Phe Tyr Glu Val Tyr Val Asn Ser Phe Tyr Asp Ala
    50                  55                  60
Asn Lys Asp Gly His Gly Asp Leu Lys Gly Leu Thr Gln Lys Leu Asp
```

```
65                  70                  75                  80
Tyr Leu Asn Asp Gly Asn Ser His Thr Lys Asn Asp Leu Gln Val Asn
                85                  90                  95
Gly Ile Trp Met Met Pro Val Asn Pro Ser Pro Ser Tyr His Lys Tyr
            100                 105                 110
Asp Val Thr Asp Tyr Tyr Asn Ile Asp Pro Gln Tyr Gly Ser Leu Gln
        115                 120                 125
Asp Phe Arg Lys Leu Met Lys Glu Ala Asp Lys Arg Asp Val Lys Val
    130                 135                 140
Ile Met Asp Leu Val Val Asn His Thr Ser Ser Glu His Pro Trp Phe
145                 150                 155                 160
Gln Ala Ala Leu Lys Asp Lys Asn Ser Lys Tyr Arg Asp Tyr Tyr Ile
                165                 170                 175
Trp Ala Asp Lys Asn Thr Asp Leu Asn Glu Lys Gly Ser Trp Gly Gln
            180                 185                 190
Gln Val Trp His Lys Ala Pro Asn Gly Glu Tyr Phe Tyr Gly Thr Phe
        195                 200                 205
Trp Glu Gly Met Pro Asp Leu Asn Tyr Asp Asn Pro Glu Val Arg Lys
    210                 215                 220
Glu Met Ile Asn Val Gly Lys Phe Trp Leu Lys Gln Gly Val Asp Gly
225                 230                 235                 240
Phe Arg Leu Asp Ala Ala Leu His Ile Phe Lys Gly Gln Thr Pro Glu
                245                 250                 255
Gly Ala Lys Lys Asn Leu Leu Trp Trp Asn Glu Phe Arg Asp Ala Met
            260                 265                 270
Lys Lys Glu Asn Pro Asn Val Tyr Leu Thr Gly Glu Val Trp Asp Gln
        275                 280                 285
Pro Glu Val Val Ala Pro Tyr Tyr Gln Ser Leu Asp Ser Leu Phe Asn
    290                 295                 300
Phe Asp Leu Ala Gly Lys Ile Val Ser Ser Val Lys Ala Gly Asn Asp
305                 310                 315                 320
Gln Gly Ile Ala Thr Ala Ala Ala Ala Thr Asp Glu Leu Phe Lys Ser
                325                 330                 335
Tyr Asn Pro Asn Lys Ile Asp Gly Ile Phe Leu Thr Asn His Asp Gln
            340                 345                 350
Asn Arg Val Met Ser Glu Leu Ser Gly Asp Val Asn Lys Ala Lys Ser
        355                 360                 365
Ala Ala Ser Ile Leu Leu Thr Leu Pro Gly Asn Pro Tyr Ile Tyr Tyr
    370                 375                 380
Gly Glu Glu Ile Gly Met Thr Gly Glu Lys Pro Asp Glu Leu Ile Arg
385                 390                 395                 400
Glu Pro Phe Arg Trp Tyr Glu Gly Asn Gly Ile Gly Gln Thr Ser Trp
                405                 410                 415
Glu Thr Pro Val Tyr Asn Lys Gly Gly Asn Gly Val Ser Val Glu Ala
            420                 425                 430
Gln Thr Lys Gln Lys Asp Ser Leu Leu Asn His Tyr Arg Glu Met Ile
        435                 440                 445
Arg Val Arg Gln Gln His Glu Glu Leu Val Lys Gly Thr Leu Gln Ser
    450                 455                 460
Ile Ser Val Asp Ser Lys Glu Val Val Ala Tyr Ser Arg Thr Tyr Lys
465                 470                 475                 480
Gly Asn Ser Ile Ser Val Tyr His Asn Ile Ser Asn Gln Pro Val Lys
                485                 490                 495
Val Ser Val Ala Ala Lys Gly Lys Leu Ile Phe Ala Ser Glu Lys Gly
            500                 505                 510
Ala Lys Lys Gly Lys Asn Gln Leu Val Ile Pro Ala Asn Ala Thr Val
        515                 520                 525
```

Leu Ile Lys
530

<210> 175
<211> 1398
<212> DNA
<213> Environmental

<400> 175
atgaaaaata taatacgact ttgtgctgcc agcgctatcc tcacggtgtc ccacgccagt 60
tacgccgacg caattttaca cgcgtttaac tggcaatata ccgatgtaac cgccaatgca 120
aatcaaattg ccgcaaatgg ctttaaaaaa gtcctcattt cacccgcaat gaaatccagc 180
ggcagtcaat ggtgggcccg ctatcaaccg caagacttgc gtgtcattga ttctccgctg 240
ggcaacaaac aagatttagt cgcgatgatc aatgcgctca acagcgttgg ggtcgacgtg 300
tatgctgacg tggtgcttaa ccatatggct aacgagtcat ggaagcgcag tgacctgaac 360
tacccgggga gtgaggtgct caacgactat caatcccgca gtgcttacta tcaaaggcaa 420
acacttttcg gcaatttaca ggagaacctt ttttccgaga atgatttcca tccggcaggc 480
tgtattacca attggaatga tcctggccac gtccagtatt ggcgcttgtg cggcggacag 540
ggcgatactg ggctaccgga tctcgatcct aatcaatggg ttgtgagtca gcagaagagt 600
tacttgaacg cactcaaatc aatgggaatc aaagggttcc gtatcgatgc ggtcaaacat 660
atgagtcaat atcaaataga ccaagtgttt accccagaca ttaccgctgg tatgcatata 720
ttcggagaag tcattaccag tggtgggcaa ggtgatagcg gctatgaggc ttttcttgcc 780
ccttacctta ataataccga tcacgccgct tatgacttcc cgctatttgc atcgattcga 840
gccgcgtttt cattctctgg tgggttaaat cagctacaca atccacaagc ctatggccaa 900
gcgttacagg actcacgtgc gatcaccttt acgattaccc acgacattcc aaccaatgac 960
ggtttccgct accagatcat ggatccaacc gatgaacagc tcgcctatgc ctacatcttg 1020
ggcaaagatg gaggaacgcc acttgtctat agtgatgacc tacctgacag cgaagacaaa 1080
gacagtggtc gttgggccga tgtgtggcaa gatccgaaca tgattaacat gcttgccttc 1140
cacaacgcga tgcaaggaca aagcatgact gtagtggcta gcgatcaatg taccttgcta 1200
tttaagcgcg gcaagcaagg cgtggtagga atcaataaat gtggcgagag taagtcggtg 1260
actgtcgata cttaccagca tgagtttaac tggtacaccc cgtaccaaga cgtattgagc 1320
ggcgacatca ccacagtgag ttctcgttat caccaatttg ttttgccagc gcgcagtgca 1380
aggatgtgga aactataa 1398

<210> 176
<211> 465
<212> PRT
<213> Environmental

<400> 176
Met Lys Asn Ile Ile Arg Leu Cys Ala Ala Ser Ala Ile Leu Thr Val
1 5 10 15
Ser His Ala Ser Tyr Ala Asp Ala Ile Leu His Ala Phe Asn Trp Gln
20 25 30
Tyr Thr Asp Val Thr Ala Asn Ala Asn Gln Ile Ala Ala Asn Gly Phe
35 40 45
Lys Lys Val Leu Ile Ser Pro Ala Met Lys Ser Ser Gly Ser Gln Trp
50 55 60
Trp Ala Arg Tyr Gln Pro Gln Asp Leu Arg Val Ile Asp Ser Pro Leu
65 70 75 80
Gly Asn Lys Gln Asp Leu Val Ala Met Ile Asn Ala Leu Asn Ser Val
85 90 95
Gly Val Asp Val Tyr Ala Asp Val Val Leu Asn His Met Ala Asn Glu
100 105 110
Ser Trp Lys Arg Ser Asp Leu Asn Tyr Pro Gly Ser Glu Val Leu Asn
115 120 125
Asp Tyr Gln Ser Arg Ser Ala Tyr Tyr Gln Arg Gln Thr Leu Phe Gly

```
    130                 135                 140
Asn Leu Gln Glu Asn Leu Phe Ser Glu Asn Asp Phe His Pro Ala Gly
145                 150                 155                 160
Cys Ile Thr Asn Trp Asn Asp Pro Gly His Val Gln Tyr Trp Arg Leu
                165                 170                 175
Cys Gly Gly Gln Gly Asp Thr Gly Leu Pro Asp Leu Asp Pro Asn Gln
            180                 185                 190
Trp Val Val Ser Gln Gln Lys Ser Tyr Leu Asn Ala Leu Lys Ser Met
        195                 200                 205
Gly Ile Lys Gly Phe Arg Ile Asp Ala Val Lys His Met Ser Gln Tyr
    210                 215                 220
Gln Ile Asp Gln Val Phe Thr Pro Asp Ile Thr Ala Gly Met His Ile
225                 230                 235                 240
Phe Gly Glu Val Ile Thr Ser Gly Gly Gln Gly Asp Ser Gly Tyr Glu
                245                 250                 255
Ala Phe Leu Ala Pro Tyr Leu Asn Asn Thr Asp His Ala Ala Tyr Asp
            260                 265                 270
Phe Pro Leu Phe Ala Ser Ile Arg Ala Ala Phe Ser Phe Ser Gly Gly
        275                 280                 285
Leu Asn Gln Leu His Asn Pro Gln Ala Tyr Gly Gln Ala Leu Gln Asp
    290                 295                 300
Ser Arg Ala Ile Thr Phe Thr Ile Thr His Asp Ile Pro Thr Asn Asp
305                 310                 315                 320
Gly Phe Arg Tyr Gln Ile Met Asp Pro Thr Asp Glu Gln Leu Ala Tyr
                325                 330                 335
Ala Tyr Ile Leu Gly Lys Asp Gly Gly Thr Pro Leu Val Tyr Ser Asp
            340                 345                 350
Asp Leu Pro Asp Ser Glu Asp Lys Asp Ser Gly Arg Trp Ala Asp Val
        355                 360                 365
Trp Gln Asp Pro Asn Met Ile Asn Met Leu Ala Phe His Asn Ala Met
    370                 375                 380
Gln Gly Gln Ser Met Thr Val Val Ala Ser Asp Gln Cys Thr Leu Leu
385                 390                 395                 400
Phe Lys Arg Gly Lys Gln Gly Val Val Gly Ile Asn Lys Cys Gly Glu
                405                 410                 415
Ser Lys Ser Val Thr Val Asp Thr Tyr Gln His Glu Phe Asn Trp Tyr
            420                 425                 430
Thr Pro Tyr Gln Asp Val Leu Ser Gly Asp Ile Thr Thr Val Ser Ser
        435                 440                 445
Arg Tyr His Gln Phe Val Leu Pro Ala Arg Ser Ala Arg Met Trp Lys
    450                 455                 460
Leu
465
```

<210> 177
<211> 1524
<212> DNA
<213> Environmental

<400> 177

```
atgaaaacat tcaaattaaa acgcactttt ttaccgctga ccttgctgct cagtgctcct      60
gcctttgctg ggcaaaatgg caccatgatg cagtattttc attggtacgt acctaatgat     120
ggcgcattat ggacgcaggt tgaaagcaat gctccagtac tcgctgaaaa cggttttaca     180
gcgctctggc taccgcccgc atacaaaggc gcgggcggca gtaatgacgt cggttatggc     240
gtctatgata tgtacgattt aggtgagttt gaccaaaaag gctcagtacg aaccaaatac     300
ggcaccaagg ctcagtacat ctctgcaatc aatgccgcgc acaacaacaa tatccaaatt     360
tacggcgacg ttgtgtttaa ccaccgaggt ggcgctgatg ggaagtcgtg ggtcgatacc     420
```

```
aagcgcgttg attgggacaa ccgcaatatt gaactgggcg acaaatggat tgaagcttgg     480
gttgagttta attttcctgg ccgcaacgac aaatactcga acttccattg gacttggtat     540
cactttgacg gtgttgactg ggatgatgcc ggcaaagaaa aagcgatctt taaattcaaa     600
ggcgaaggaa aagcatggga ttgggaagtc agctctgaaa aaggcaatta cgactaccta     660
atgtacgccg atttagacat ggatcaccca gaagttaaac aagagctgaa agattggggt     720
gagtggtaca tcaacatgac cggcgttgat ggctttagaa tggatgccgt gaagcacatt     780
aaatatcagt atctacaaga gtggattgat catttacgtt ggaaaacagg caaagagctt     840
ttcaccgttg gtgagtattg gaattacgac gtaaatcaac tgcacaactt tattactaag     900
acctctggca gtatgtcgtt gttcgatgcg ccgcttcaca tgaatttcta caacgcgtca     960
aaatctggcg gcacttacga tatgcgccaa atcatgaatg gcacgttgat gaaggacaac    1020
ccagtcaaag cagtgactct cgtagaaaac cacgatacgc agccattgca ggcgttagag    1080
tcgacagtag attggtggtt caagcctctt gcttacgcat tcattttatt gcgtgaagaa    1140
ggttatccat cggtgttcta cgcagattac tacggcgcgc agtacagcga caaaggttac    1200
aacattaata tggccaaagt gccttacatt gaagaacttg taacactgcg taaagagtat    1260
gcgtatggca aacagaattc ttatctcgac cattgggatg tgattggctg gacccgagag    1320
ggcgatgctg aacatccaaa ctcaatggcg gtgatcatga gtgatggacc gggcggcaca    1380
aaatggatgt ataccggtaa gccaagtacg cgctatgtcg acaagctggg tatccgaact    1440
gaagatgttt ggaccgatgc caatggctgg gcagaatttc ctgtcaatgg tggttcagtc    1500
tcggtttggg tgggcgttaa gtaa                                           1524
```

<210> 178
<211> 507
<212> PRT
<213> Environmental

<400> 178

```
Met Lys Thr Phe Lys Leu Lys Arg Thr Phe Leu Pro Leu Thr Leu Leu
 1               5                  10                  15
Leu Ser Ala Pro Ala Phe Ala Gly Gln Asn Gly Thr Met Met Gln Tyr
            20                  25                  30
Phe His Trp Tyr Val Pro Asn Asp Gly Ala Leu Trp Thr Gln Val Glu
        35                  40                  45
Ser Asn Ala Pro Val Leu Ala Glu Asn Gly Phe Thr Ala Leu Trp Leu
    50                  55                  60
Pro Pro Ala Tyr Lys Gly Ala Gly Gly Ser Asn Asp Val Gly Tyr Gly
65                  70                  75                  80
Val Tyr Asp Met Tyr Asp Leu Gly Glu Phe Asp Gln Lys Gly Ser Val
                85                  90                  95
Arg Thr Lys Tyr Gly Thr Lys Ala Gln Tyr Ile Ser Ala Ile Asn Ala
            100                 105                 110
Ala His Asn Asn Asn Ile Gln Ile Tyr Gly Asp Val Val Phe Asn His
        115                 120                 125
Arg Gly Gly Ala Asp Gly Lys Ser Trp Val Asp Thr Lys Arg Val Asp
    130                 135                 140
Trp Asp Asn Arg Asn Ile Glu Leu Gly Asp Lys Trp Ile Glu Ala Trp
145                 150                 155                 160
Val Glu Phe Asn Phe Pro Gly Arg Asn Asp Lys Tyr Ser Asn Phe His
                165                 170                 175
Trp Thr Trp Tyr His Phe Asp Gly Val Asp Trp Asp Asp Ala Gly Lys
            180                 185                 190
Glu Lys Ala Ile Phe Lys Phe Lys Gly Glu Gly Lys Ala Trp Asp Trp
        195                 200                 205
Glu Val Ser Ser Glu Lys Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp
    210                 215                 220
Leu Asp Met Asp His Pro Glu Val Lys Gln Glu Leu Lys Asp Trp Gly
225                 230                 235                 240
Glu Trp Tyr Ile Asn Met Thr Gly Val Asp Gly Phe Arg Met Asp Ala
```

```
                245                 250                 255
Val Lys His Ile Lys Tyr Gln Tyr Leu Gln Glu Trp Ile Asp His Leu
            260                 265                 270
Arg Trp Lys Thr Gly Lys Glu Leu Phe Thr Val Gly Glu Tyr Trp Asn
        275                 280                 285
Tyr Asp Val Asn Gln Leu His Asn Phe Ile Thr Lys Thr Ser Gly Ser
    290                 295                 300
Met Ser Leu Phe Asp Ala Pro Leu His Met Asn Phe Tyr Asn Ala Ser
305                 310                 315                 320
Lys Ser Gly Gly Thr Tyr Asp Met Arg Gln Ile Met Asn Gly Thr Leu
                325                 330                 335
Met Lys Asp Asn Pro Val Lys Ala Val Thr Leu Val Glu Asn His Asp
            340                 345                 350
Thr Gln Pro Leu Gln Ala Leu Glu Ser Thr Val Asp Trp Trp Phe Lys
        355                 360                 365
Pro Leu Ala Tyr Ala Phe Ile Leu Leu Arg Glu Glu Gly Tyr Pro Ser
    370                 375                 380
Val Phe Tyr Ala Asp Tyr Tyr Gly Ala Gln Tyr Ser Asp Lys Gly Tyr
385                 390                 395                 400
Asn Ile Asn Met Ala Lys Val Pro Tyr Ile Glu Glu Leu Val Thr Leu
                405                 410                 415
Arg Lys Glu Tyr Ala Tyr Gly Lys Gln Asn Ser Tyr Leu Asp His Trp
            420                 425                 430
Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Ala Glu His Pro Asn Ser
        435                 440                 445
Met Ala Val Ile Met Ser Asp Gly Pro Gly Gly Thr Lys Trp Met Tyr
    450                 455                 460
Thr Gly Lys Pro Ser Thr Arg Tyr Val Asp Lys Leu Gly Ile Arg Thr
465                 470                 475                 480
Glu Asp Val Trp Thr Asp Ala Asn Gly Trp Ala Glu Phe Pro Val Asn
                485                 490                 495
Gly Gly Ser Val Ser Val Trp Val Gly Val Lys
            500                 505
```

<210> 179
<211> 1524
<212> DNA
<213> Environmental

<400> 179

```
atgaaaacat tcaaattaaa acgcactttt ttaccgctaa ccttgctgct cagtgctcct      60
gcctttgccg ggcaaaatgg caccatgatg cagtactttc attggtacgt acctaatgat     120
ggcgcattat ggacgcaggt tgaaagcaat gctccagcac tcgctgaaaa cggttttaca     180
gcgctctggc taccgccagc ttacaaaggc gcgggcggca gtaatgatgt cggttatggc     240
gtctacgata tgtacgattt aggtgagttt gatcaaaaag gctcagtacg aaccaaatac     300
ggtaccaagg ctcagtacat ctctgcaatc aatgctgcgc acaacaacaa tatccaaatt     360
tacggcgacg ttgtgtttaa ccatcgtggt ggcgctgatg ggaagtcgtg ggtcgatacc     420
aagcgcgttg attgggacaa ccgtaacatt gaactgggcg acaaatggat tgaagcttgg     480
gttgagttta attttcctag ccgcaacgac aaatactcga acttccattg gacttggtat     540
cactttgacg gtgttgactg ggatgatgcc ggcaaagaaa aagcgatctt taaattcaaa     600
ggcgaaggaa aagcatggga ttgggaagtc agctctgaaa aaggcaatta cgactaccta     660
atgtacgccg atttagacat ggatcaccca gaagttaaac aagagctgaa agattggggt     720
gagtggtaca tcaacatgac cggcgttgat ggctttagaa tggatgccgt taagcacatt     780
aaatatcagt atctacaaga gtggattgat catttacgtt ggaaaacagg caaagagctt     840
ttcaccgttg gtgagtattg gaattacgac gtaaatcaac tgcataactt tattactaag     900
acctctggca gtatgtcgtt gttcgatgcg ccgcttcaca tgaacttcta caacgcgtca     960
aaatctggcg gcaattacga tatgcgccaa atcatgaatg gcacgttgat gaaggacaac    1020
```

```
ccagtcaaag ctgtgactct cgtagaaaac cacgatacgc agccattgca ggcgttagag    1080
tcgacagtgg attggtggtt caagcctctt gcttacgcat tcatcttgtt gcgtgaagaa    1140
ggttatccat cggtgttcta cgcagattac tacggcgcgc agtacagcga caaaggttac    1200
aacattaata tggccaaagt gccttacatt gaagaacttg taacactgcg taaagagtat    1260
gcgtatggca aacagaattc ttatctcgac cattgggatg tgattggctg gactcgagag    1320
ggcgatgctg aacatccaaa ctcaatggcg gtgatcatga gtgatggacc gggcggaaca    1380
aaatggatgt ataccggtaa tccaagcacg cgctatgtcg acaagctggg tatccgaact    1440
gaagatgttt ggaccgatgc caatggctgg gcagaatttc ctgtcaatgg tggttcagtc    1500
tcggtttggg tgggcgttaa gtaa                                           1524

<210> 180
<211> 507
<212> PRT
<213> Environmental

<400> 180
Met Lys Thr Phe Lys Leu Lys Arg Thr Phe Leu Pro Leu Thr Leu Leu
 1               5                  10                  15
Leu Ser Ala Pro Ala Phe Ala Gly Gln Asn Gly Thr Met Met Gln Tyr
            20                  25                  30
Phe His Trp Tyr Val Pro Asn Asp Gly Ala Leu Trp Thr Gln Val Glu
        35                  40                  45
Ser Asn Ala Pro Ala Leu Ala Glu Asn Gly Phe Thr Ala Leu Trp Leu
    50                  55                  60
Pro Pro Ala Tyr Lys Gly Ala Gly Gly Ser Asn Asp Val Gly Tyr Gly
65                  70                  75                  80
Val Tyr Asp Met Tyr Asp Leu Gly Glu Phe Asp Gln Lys Gly Ser Val
                85                  90                  95
Arg Thr Lys Tyr Gly Thr Lys Ala Gln Tyr Ile Ser Ala Ile Asn Ala
            100                 105                 110
Ala His Asn Asn Asn Ile Gln Ile Tyr Gly Asp Val Val Phe Asn His
        115                 120                 125
Arg Gly Gly Ala Asp Gly Lys Ser Trp Val Asp Thr Lys Arg Val Asp
    130                 135                 140
Trp Asp Asn Arg Asn Ile Glu Leu Gly Asp Lys Trp Ile Glu Ala Trp
145                 150                 155                 160
Val Glu Phe Asn Phe Pro Ser Arg Asn Asp Lys Tyr Ser Asn Phe His
                165                 170                 175
Trp Thr Trp Tyr His Phe Asp Gly Val Asp Trp Asp Asp Ala Gly Lys
            180                 185                 190
Glu Lys Ala Ile Phe Lys Phe Lys Gly Glu Gly Lys Ala Trp Asp Trp
        195                 200                 205
Glu Val Ser Ser Glu Lys Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp
    210                 215                 220
Leu Asp Met Asp His Pro Glu Val Lys Gln Glu Leu Lys Asp Trp Gly
225                 230                 235                 240
Glu Trp Tyr Ile Asn Met Thr Gly Val Asp Gly Phe Arg Met Asp Ala
                245                 250                 255
Val Lys His Ile Lys Tyr Gln Tyr Leu Gln Glu Trp Ile Asp His Leu
            260                 265                 270
Arg Trp Lys Thr Gly Lys Glu Leu Phe Thr Val Gly Glu Tyr Trp Asn
        275                 280                 285
Tyr Asp Val Asn Gln Leu His Asn Phe Ile Thr Lys Thr Ser Gly Ser
    290                 295                 300
Met Ser Leu Phe Asp Ala Pro Leu His Met Asn Phe Tyr Asn Ala Ser
305                 310                 315                 320
Lys Ser Gly Gly Asn Tyr Asp Met Arg Gln Ile Met Asn Gly Thr Leu
```

```
                325                 330                 335
Met Lys Asp Asn Pro Val Lys Ala Val Thr Leu Val Glu Asn His Asp
            340                 345                 350
Thr Gln Pro Leu Gln Ala Leu Glu Ser Thr Val Asp Trp Trp Phe Lys
        355                 360                 365
Pro Leu Ala Tyr Ala Phe Ile Leu Leu Arg Glu Glu Gly Tyr Pro Ser
    370                 375                 380
Val Phe Tyr Ala Asp Tyr Tyr Gly Ala Gln Tyr Ser Asp Lys Gly Tyr
385                 390                 395                 400
Asn Ile Asn Met Ala Lys Val Pro Tyr Ile Glu Glu Leu Val Thr Leu
                405                 410                 415
Arg Lys Glu Tyr Ala Tyr Gly Lys Gln Asn Ser Tyr Leu Asp His Trp
            420                 425                 430
Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Ala Glu His Pro Asn Ser
        435                 440                 445
Met Ala Val Ile Met Ser Asp Gly Pro Gly Gly Thr Lys Trp Met Tyr
    450                 455                 460
Thr Gly Asn Pro Ser Thr Arg Tyr Val Asp Lys Leu Gly Ile Arg Thr
465                 470                 475                 480
Glu Asp Val Trp Thr Asp Ala Asn Gly Trp Ala Glu Phe Pro Val Asn
                485                 490                 495
Gly Gly Ser Val Ser Val Trp Val Gly Val Lys
            500                 505
```

<210> 181
<211> 1830
<212> DNA
<213> Environmental

<400> 181

```
atgccagagg ccttcggcct ggccattacg ccgtcacata gccggcgggg gaggttggtg      60
ggcgtgtcgc gcgggggcag cctgccgatg ccggtcctcc actggccggc gttcatcctc     120
gtccggcgct tcgtcgccgg tcatccgaac aagcacaaga accggagtat tgcgatgagc     180
cacaccctgc gtgccgccgt attggcggcg atcctgctgc cgttccccgc cctcgctgac     240
caggccggca agagcccggc cggcgtgcgc taccacggcg gcgacgaaat catcctccag     300
ggcttccact ggaacgtcgt ccgcgaagcg cccaacgact ggtacaacat ccttcgccag     360
caggcctcga cgatcgccgc ggacggcttc tcggcaatct ggatgccggt gccctggcgt     420
gacttctcca gctggaccga cggcggcaag tcaggcggcg gcgaaggcta cttctggcac     480
gacttcaaca agaacggccg ctacggcagc gacgcccagc tgcgccaggc cgccggcgca     540
ctcggtggcg ccggggtgaa ggtgctctac gatgtggtgc ccaatcacat gaaccgcggc     600
tatccggaca aggagatcaa cctgccggcc ggccagggct tctggcgcaa cgactgcacc     660
gacccgggca actaccccaa cgactgcgat gacggtgacc gcttcatcgg cggcaagtcg     720
gacctgaaca ccggccatcc gcagatctac ggcatgtttc gcgacgagct tgccaacctg     780
cgcagcgggt acggcgccgg cggcttccgc ttcgacttcg ttcgcggcta tgcgcccgaa     840
cgggtcgaca gctggatgag cgacagcgcc gacagcagtt tctgcgttgg cgagctgtgg     900
aaaagcccgt ccgagtaccc gagctgggac tggcgcaaca cggcgagctg gcagcagatc     960
atcaaggact ggtccgaccg ggccaagtgc ccggtgttcg acttcgcgct caaggagcgc    1020
atgcagaacg gctcggtcgc cgactggaag catggcctca atggcaaccc ggacccgcgc    1080
tggcgcgagg tggcggtgac ctttgtcgac aaccacgaca ccggctattc gcccgggcag    1140
aacggcggcc agcaccactg ggcgctgcag gacgggctga tccgccaggc ctacgcctac    1200
atcctcacca gcccgggcac gccggtggtg tactggtcgc acatgtacga ctggggctac    1260
ggcgacttca ttcgccagct gatccaggtg cggcgcaccg ctggcgtgcg cgccgattcg    1320
gcgatcagct tccacagcgg ctacagcggc ctggtcgcta ccgtcagcgg cagccatcag    1380
accctggtgg tggcgctcaa ctccgatctg gccaaccccg gccaggtcgc cagcggcagc    1440
ttcagcgagg cggtcaacgc cagcaacggc caggtgcgcg tctggcgcag cggtagcggc    1500
gatggcggcg gcaatgacgg cggcgagggc ggtctggtca atgtgaactt ccgctgcgac    1560
aacggcgtga cgcagatggg cgacagcgtc tacgcggtgg gcaacgtcag ccagctcggc    1620
```

```
aactggagcc cggcctccgc ggtacggctg accgacacca gcagctatcc gacctggaag    1680
ggcagcatcg ccctgcctga cggtcagaac gtggaatgga agtgcctgat ccgtaacgag    1740
gcggacgcga cgctggtgcg ccagtggcaa tcgggcggca acaaccaggt ccaggccgct    1800
gccggcgcga gcaccagcgg ctcgttctga                                     1830

<210> 182
<211> 609
<212> PRT
<213> Environmental

<400> 182
Met Pro Glu Ala Phe Gly Leu Ala Ile Thr Pro Ser His Ser Arg Arg
 1               5                  10                  15
Gly Arg Leu Val Gly Val Ser Arg Gly Gly Ser Leu Pro Met Pro Val
            20                  25                  30
Leu His Trp Pro Ala Phe Ile Leu Val Arg Arg Phe Val Ala Gly His
        35                  40                  45
Pro Asn Lys His Lys Asn Arg Ser Ile Ala Met Ser His Thr Leu Arg
    50                  55                  60
Ala Ala Val Leu Ala Ala Ile Leu Leu Pro Phe Pro Ala Leu Ala Asp
65                  70                  75                  80
Gln Ala Gly Lys Ser Pro Ala Gly Val Arg Tyr His Gly Gly Asp Glu
                85                  90                  95
Ile Ile Leu Gln Gly Phe His Trp Asn Val Val Arg Glu Ala Pro Asn
            100                 105                 110
Asp Trp Tyr Asn Ile Leu Arg Gln Gln Ala Ser Thr Ile Ala Ala Asp
        115                 120                 125
Gly Phe Ser Ala Ile Trp Met Pro Val Pro Trp Arg Asp Phe Ser Ser
    130                 135                 140
Trp Thr Asp Gly Gly Lys Ser Gly Gly Gly Glu Gly Tyr Phe Trp His
145                 150                 155                 160
Asp Phe Asn Lys Asn Gly Arg Tyr Gly Ser Asp Ala Gln Leu Arg Gln
                165                 170                 175
Ala Ala Gly Ala Leu Gly Gly Ala Gly Val Lys Val Leu Tyr Asp Val
            180                 185                 190
Val Pro Asn His Met Asn Arg Gly Tyr Pro Asp Lys Glu Ile Asn Leu
        195                 200                 205
Pro Ala Gly Gln Gly Phe Trp Arg Asn Asp Cys Thr Asp Pro Gly Asn
    210                 215                 220
Tyr Pro Asn Asp Cys Asp Asp Gly Asp Arg Phe Ile Gly Gly Lys Ser
225                 230                 235                 240
Asp Leu Asn Thr Gly His Pro Gln Ile Tyr Gly Met Phe Arg Asp Glu
                245                 250                 255
Leu Ala Asn Leu Arg Ser Gly Tyr Gly Ala Gly Gly Phe Arg Phe Asp
            260                 265                 270
Phe Val Arg Gly Tyr Ala Pro Glu Arg Val Asp Ser Trp Met Ser Asp
        275                 280                 285
Ser Ala Asp Ser Ser Phe Cys Val Gly Glu Leu Trp Lys Ser Pro Ser
    290                 295                 300
Glu Tyr Pro Ser Trp Asp Trp Arg Asn Thr Ala Ser Trp Gln Gln Ile
305                 310                 315                 320
Ile Lys Asp Trp Ser Asp Arg Ala Lys Cys Pro Val Phe Asp Phe Ala
                325                 330                 335
Leu Lys Glu Arg Met Gln Asn Gly Ser Val Ala Asp Trp Lys His Gly
            340                 345                 350
Leu Asn Gly Asn Pro Asp Pro Arg Trp Arg Glu Val Ala Val Thr Phe
        355                 360                 365
```

```
Val Asp Asn His Asp Thr Gly Tyr Ser Pro Gly Gln Asn Gly Gly Gln
    370                 375                 380
His His Trp Ala Leu Gln Asp Gly Leu Ile Arg Gln Ala Tyr Ala Tyr
385                 390                 395                 400
Ile Leu Thr Ser Pro Gly Thr Pro Val Val Tyr Trp Ser His Met Tyr
                405                 410                 415
Asp Trp Gly Tyr Gly Asp Phe Ile Arg Gln Leu Ile Gln Val Arg Arg
            420                 425                 430
Thr Ala Gly Val Arg Ala Asp Ser Ala Ile Ser Phe His Ser Gly Tyr
        435                 440                 445
Ser Gly Leu Val Ala Thr Val Ser Gly Ser His Gln Thr Leu Val Val
    450                 455                 460
Ala Leu Asn Ser Asp Leu Ala Asn Pro Gly Gln Val Ala Ser Gly Ser
465                 470                 475                 480
Phe Ser Glu Ala Val Asn Ala Ser Asn Gly Gln Val Arg Val Trp Arg
                485                 490                 495
Ser Gly Ser Gly Asp Gly Gly Gly Asn Asp Gly Gly Glu Gly Gly Leu
            500                 505                 510
Val Asn Val Asn Phe Arg Cys Asp Asn Gly Val Thr Gln Met Gly Asp
        515                 520                 525
Ser Val Tyr Ala Val Gly Asn Val Ser Gln Leu Gly Asn Trp Ser Pro
    530                 535                 540
Ala Ser Ala Val Arg Leu Thr Asp Thr Ser Ser Tyr Pro Thr Trp Lys
545                 550                 555                 560
Gly Ser Ile Ala Leu Pro Asp Gly Gln Asn Val Glu Trp Lys Cys Leu
                565                 570                 575
Ile Arg Asn Glu Ala Asp Ala Thr Leu Val Arg Gln Trp Gln Ser Gly
            580                 585                 590
Gly Asn Asn Gln Val Gln Ala Ala Ala Gly Ala Ser Thr Ser Gly Ser
        595                 600                 605
Phe
```

<210> 183
<211> 1596
<212> DNA
<213> Environmental

<400> 183

```
atgcaaacga ttgcaaaaaa aggggatgaa acgatgaaag ggaaaaaatg gacagcttta      60
gctctaacac tgccgctggc tgctagctta tcaacaggcg ttcacgccga aaccgtacat     120
aaaggtaagt ctgaagcaac agataaaaac ggtgtctttt atgaggtgta tgtaaactct     180
ttttacgata caaataaaga tggacatggt gatttaaaag gtctgacaca aaagttggat     240
tatttaaatg acggcaattc tcatacaaag aatgatcttc aagtaaacgg gatttggatg     300
atgccagtca acccttctcc tagctatcat aaatatgatg taacggacta ttataacatt     360
gatcctcagt acggaaatct gcaagatttt cgcaagctga tgaaagaagc agacaaacga     420
gacgtaaaag tcattatgga ccttgttgtg aatcatacga gcagcgaaca cccttggttt     480
caagctgcat taaaagataa aaacagcaag tacagagatt actatatttg ggctgataaa     540
aataccgatt tgaatgaaaa aggatcttgg gggcagcaag tatggcataa agctccaaac     600
ggagagtatt tttacggaac gttttgggaa ggaatgcctg acttaaatta cgataaccct     660
gaagtaagaa aagaaatgat taacgtcgga aagttttggc taaagcaagg cgttaatggc     720
ttccgcttag atgctgcgct tcatattttt aaaggtcaaa cacctgaagg cgctaagaaa     780
aatatcctgt ggtggaatga gtttagagat gcgatgaaaa aagaaaaccc taacgtatat     840
ctaacgggtg aagtatggga tcagcctgaa gtggtagctc cttactatca atcgcttgat     900
tctttattta attttgattt agcaggaaaa attgtcagct ctgtaaaagc aggaaatgat     960
caaggaatcg ccactgcagc agcggcaaca gatgaactgt tcaaatcata caatccaaat    1020
aaaattgacg gcattttctt aaccaaccat gaccaaaatc gcgtcatgag tgagctgagc    1080
```

```
ggcgatgtga acaaagcaaa atcagctgct tctatcttac ttacgcttcc tggcaacccg    1140
tatatttatt acggtgaaga aattggcatg accggtgaaa agcctgatga gttaatccgt    1200
gaaccattcc gctggtacga aggaaacgga cttggacaaa ctagctggga aacacctgta    1260
tataacaaag gcggcaacgg cgtgtctgta gaagtacaaa ccaaacaaaa ggattctttg    1320
ttaaatcatt atcgtgaaat gattcgcgtg cgtcagcagc atgaagagtt agtaaaagga    1380
acgcttcaat ctatttcagt agacagtaaa gaagtggttg cctatagtcg cacgtataaa    1440
ggcaactcga ttagcgtgta tcataatatt tcaaatcaac ctgtaaaagt atctgtagca    1500
gcgaaaggta aattgatttt tgctagtgaa aaaggtgcta aaaaagtcaa aaatcagctt    1560
gtaattccgg ctaatacaac ggttttaata aaataa                              1596
```

<210> 184
<211> 531
<212> PRT
<213> Environmental

<400> 184

```
Met Gln Thr Ile Ala Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys
 1               5                  10                  15
Trp Thr Ala Leu Ala Leu Thr Leu Pro Leu Ala Ala Ser Leu Ser Thr
            20                  25                  30
Gly Val His Ala Glu Thr Val His Lys Gly Lys Ser Glu Ala Thr Asp
        35                  40                  45
Lys Asn Gly Val Phe Tyr Glu Val Tyr Val Asn Ser Phe Tyr Asp Thr
    50                  55                  60
Asn Lys Asp Gly His Gly Asp Leu Lys Gly Leu Thr Gln Lys Leu Asp
65                  70                  75                  80
Tyr Leu Asn Asp Gly Asn Ser His Thr Lys Asn Asp Leu Gln Val Asn
                85                  90                  95
Gly Ile Trp Met Met Pro Val Asn Pro Ser Pro Ser Tyr His Lys Tyr
            100                 105                 110
Asp Val Thr Asp Tyr Tyr Asn Ile Asp Pro Gln Tyr Gly Asn Leu Gln
        115                 120                 125
Asp Phe Arg Lys Leu Met Lys Glu Ala Asp Lys Arg Asp Val Lys Val
    130                 135                 140
Ile Met Asp Leu Val Val Asn His Thr Ser Ser Glu His Pro Trp Phe
145                 150                 155                 160
Gln Ala Ala Leu Lys Asp Lys Asn Ser Lys Tyr Arg Asp Tyr Tyr Ile
                165                 170                 175
Trp Ala Asp Lys Asn Thr Asp Leu Asn Glu Lys Gly Ser Trp Gly Gln
            180                 185                 190
Gln Val Trp His Lys Ala Pro Asn Gly Glu Tyr Phe Tyr Gly Thr Phe
        195                 200                 205
Trp Glu Gly Met Pro Asp Leu Asn Tyr Asp Asn Pro Glu Val Arg Lys
    210                 215                 220
Glu Met Ile Asn Val Gly Lys Phe Trp Leu Lys Gln Gly Val Asn Gly
225                 230                 235                 240
Phe Arg Leu Asp Ala Ala Leu His Ile Phe Lys Gly Gln Thr Pro Glu
                245                 250                 255
Gly Ala Lys Lys Asn Ile Leu Trp Trp Asn Glu Phe Arg Asp Ala Met
            260                 265                 270
Lys Lys Glu Asn Pro Asn Val Tyr Leu Thr Gly Glu Val Trp Asp Gln
        275                 280                 285
Pro Glu Val Val Ala Pro Tyr Tyr Gln Ser Leu Asp Ser Leu Phe Asn
    290                 295                 300
Phe Asp Leu Ala Gly Lys Ile Val Ser Ser Val Lys Ala Gly Asn Asp
305                 310                 315                 320
Gln Gly Ile Ala Thr Ala Ala Ala Ala Thr Asp Glu Leu Phe Lys Ser
```

```
                325                 330                 335
Tyr Asn Pro Asn Lys Ile Asp Gly Ile Phe Leu Thr Asn His Asp Gln
            340                 345                 350
Asn Arg Val Met Ser Glu Leu Ser Gly Asp Val Asn Lys Ala Lys Ser
        355                 360                 365
Ala Ala Ser Ile Leu Leu Thr Leu Pro Gly Asn Pro Tyr Ile Tyr Tyr
    370                 375                 380
Gly Glu Glu Ile Gly Met Thr Gly Glu Lys Pro Asp Glu Leu Ile Arg
385                 390                 395                 400
Glu Pro Phe Arg Trp Tyr Glu Gly Asn Gly Leu Gly Gln Thr Ser Trp
                405                 410                 415
Glu Thr Pro Val Tyr Asn Lys Gly Gly Asn Gly Val Ser Val Glu Val
            420                 425                 430
Gln Thr Lys Gln Lys Asp Ser Leu Leu Asn His Tyr Arg Glu Met Ile
        435                 440                 445
Arg Val Arg Gln Gln His Glu Glu Leu Val Lys Gly Thr Leu Gln Ser
    450                 455                 460
Ile Ser Val Asp Ser Lys Glu Val Val Ala Tyr Ser Arg Thr Tyr Lys
465                 470                 475                 480
Gly Asn Ser Ile Ser Val Tyr His Asn Ile Ser Asn Gln Pro Val Lys
                485                 490                 495
Val Ser Val Ala Ala Lys Gly Lys Leu Ile Phe Ala Ser Glu Lys Gly
            500                 505                 510
Ala Lys Lys Val Lys Asn Gln Leu Val Ile Pro Ala Asn Thr Thr Val
        515                 520                 525
Leu Ile Lys
    530
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<210> 185
<211> 1572
<212> DNA
<213> Environmental

<400> 185

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atgaaactga tgaaagggaa aaaatggaca gctttagctc taacactgcc gctggctgct      60
agcttatcaa caggcgttca cgccgaaact gtacataaag gtaaagctcc aacagcagat     120
aaaaacggtg tcttttatga ggtgtatgta aactcttttt acgatgcaaa taaagatgga     180
catggtgatt taaaaggtct tacacaaaag ctggactatt taaatgacgg aaattctcat     240
acaaagaatg atcttcaagt aaacgggatt tggatgatgc cagtcaaccc ttctcctagc     300
tatcataaat atgatgtaac ggattattat aacattgatc cgcagtacgg aaatctgcaa     360
gattttcgca agctgatgaa agaagcagac aaacgagacg taaaagtcat tatggacctt     420
gttgtgaatc atacgagcag cgaacaccct tggtttcaag ctgcgttaaa agataaaaac     480
agcaagtaca gagattacta tatttgggct gataaaaata ccgacttgaa tgaaaaagga     540
tcttggggac agcaagtatg gcataaagct ccaaacggag agtattttta cggaacgttt     600
tgggaaggaa tgcctgactt aaattacgat aaccctgaag taagaaaaga aatgattaac     660
gtcggaaagt tttggctaaa gcaaggcgtt gatggcttcc gcttagatgc tgcgcttcat     720
atttttaaag gtcaaacgcc tgaaggcgct aagaaaaata ttctgtggtg gaatgagttt     780
agagatgcga tgaaaaaaga aaaccctaac gtatatctaa cgggtgaagt atgggatcag     840
cctgaagtgg tagctcctta ctatcaatcg cttgattccc tatttaactt tgatttagca     900
gggaaaattg tcagttctgt aaaagcagga aatgatcaag gaatcgccac tgcagcagcg     960
gcaacggatg agctgttcaa atcatacaat ccaaataaaa ttgacggcat tttcttaacc    1020
aaccatgacc aaaaccgcgt catgagtgaa ctgatcggcg atgtgaacaa agcaaaatca    1080
gctgcttcta tcttacttac gcttcctggc aacccgtata tttattacgg tgaagaaatt    1140
ggcatgaccg gtgaaaagcc tgatgagtta atccgtgaac cgttccgctg gtacgaagga    1200
aacggacttg gacaaaccag ctgggaaaca cctgtatata acaaaggcgg caacggcgtg    1260
tctgtagaag cacaaaccaa acaaaaggat tctttgttaa atcattaccg tgaaatgatt    1320
cgcgtgcgtc agcagcatga agagttagta aaaggaacgc ttcaatctat tttagtagac    1380
```

agtaaagaag ttgttgccta tagccgtacg tataaagaca actcgattag cgtgtatcat 1440
aatatttcaa atcaaccggt aaaagtatct gtagcagcaa aaggtaaatt aatttttgct 1500
agtgaaaaag gtgctaaaaa agtcaagaat cagcttgtga ttccggctaa tacaacggtt 1560
ttaataaaat aa 1572

<210> 186
<211> 523
<212> PRT
<213> Environmental

<400> 186

Met	Lys	Leu	Met	Lys	Gly	Lys	Lys	Trp	Thr	Ala	Leu	Ala	Leu	Thr	Leu
1			5					10						15	
Pro	Leu	Ala	Ala	Ser	Leu	Ser	Thr	Gly	Val	His	Ala	Glu	Thr	Val	His
			20					25					30		
Lys	Gly	Lys	Ala	Pro	Thr	Ala	Asp	Lys	Asn	Gly	Val	Phe	Tyr	Glu	Val
		35					40					45			
Tyr	Val	Asn	Ser	Phe	Tyr	Asp	Ala	Asn	Lys	Asp	Gly	His	Gly	Asp	Leu
	50					55					60				
Lys	Gly	Leu	Thr	Gln	Lys	Leu	Asp	Tyr	Leu	Asn	Asp	Gly	Asn	Ser	His
65					70					75					80
Thr	Lys	Asn	Asp	Leu	Gln	Val	Asn	Gly	Ile	Trp	Met	Met	Pro	Val	Asn
				85					90					95	
Pro	Ser	Pro	Ser	Tyr	His	Lys	Tyr	Asp	Val	Thr	Asp	Tyr	Tyr	Asn	Ile
			100					105					110		
Asp	Pro	Gln	Tyr	Gly	Asn	Leu	Gln	Asp	Phe	Arg	Lys	Leu	Met	Lys	Glu
		115					120					125			
Ala	Asp	Lys	Arg	Asp	Val	Lys	Val	Ile	Met	Asp	Leu	Val	Val	Asn	His
	130					135					140				
Thr	Ser	Ser	Glu	His	Pro	Trp	Phe	Gln	Ala	Ala	Leu	Lys	Asp	Lys	Asn
145					150					155					160
Ser	Lys	Tyr	Arg	Asp	Tyr	Tyr	Ile	Trp	Ala	Asp	Lys	Asn	Thr	Asp	Leu
				165					170					175	
Asn	Glu	Lys	Gly	Ser	Trp	Gly	Gln	Gln	Val	Trp	His	Lys	Ala	Pro	Asn
			180					185					190		
Gly	Glu	Tyr	Phe	Tyr	Gly	Thr	Phe	Trp	Glu	Gly	Met	Pro	Asp	Leu	Asn
		195					200					205			
Tyr	Asp	Asn	Pro	Glu	Val	Arg	Lys	Glu	Met	Ile	Asn	Val	Gly	Lys	Phe
	210					215					220				
Trp	Leu	Lys	Gln	Gly	Val	Asp	Gly	Phe	Arg	Leu	Asp	Ala	Ala	Leu	His
225					230					235					240
Ile	Phe	Lys	Gly	Gln	Thr	Pro	Glu	Gly	Ala	Lys	Lys	Asn	Ile	Leu	Trp
				245					250					255	
Trp	Asn	Glu	Phe	Arg	Asp	Ala	Met	Lys	Lys	Glu	Asn	Pro	Asn	Val	Tyr
			260					265					270		
Leu	Thr	Gly	Glu	Val	Trp	Asp	Gln	Pro	Glu	Val	Val	Ala	Pro	Tyr	Tyr
		275					280					285			
Gln	Ser	Leu	Asp	Ser	Leu	Phe	Asn	Phe	Asp	Leu	Ala	Gly	Lys	Ile	Val
	290					295					300				
Ser	Ser	Val	Lys	Ala	Gly	Asn	Asp	Gln	Gly	Ile	Ala	Thr	Ala	Ala	Ala
305					310					315					320
Ala	Thr	Asp	Glu	Leu	Phe	Lys	Ser	Tyr	Asn	Pro	Asn	Lys	Ile	Asp	Gly
				325					330					335	
Ile	Phe	Leu	Thr	Asn	His	Asp	Gln	Asn	Arg	Val	Met	Ser	Glu	Leu	Ile
			340					345					350		
Gly	Asp	Val	Asn	Lys	Ala	Lys	Ser	Ala	Ala	Ser	Ile	Leu	Leu	Thr	Leu
		355					360					365			

```
Pro Gly Asn Pro Tyr Ile Tyr Tyr Gly Glu Glu Ile Gly Met Thr Gly
    370                 375                 380
Glu Lys Pro Asp Glu Leu Ile Arg Glu Pro Phe Arg Trp Tyr Glu Gly
385                 390                 395                 400
Asn Gly Leu Gly Gln Thr Ser Trp Glu Thr Pro Val Tyr Asn Lys Gly
                405                 410                 415
Gly Asn Gly Val Ser Val Glu Ala Gln Thr Lys Gln Lys Asp Ser Leu
            420                 425                 430
Leu Asn His Tyr Arg Glu Met Ile Arg Val Arg Gln Gln His Glu Glu
        435                 440                 445
Leu Val Lys Gly Thr Leu Gln Ser Ile Leu Val Asp Ser Lys Glu Val
    450                 455                 460
Val Ala Tyr Ser Arg Thr Tyr Lys Asp Asn Ser Ile Ser Val Tyr His
465                 470                 475                 480
Asn Ile Ser Asn Gln Pro Val Lys Val Ser Val Ala Ala Lys Gly Lys
                485                 490                 495
Leu Ile Phe Ala Ser Glu Lys Gly Ala Lys Lys Val Lys Asn Gln Leu
            500                 505                 510
Val Ile Pro Ala Asn Thr Thr Val Leu Ile Lys
        515                 520
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<210> 187
<211> 2052
<212> DNA
<213> Environmental

<400> 187

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atgtatctca tccaggaggg gcacatgcgt tttccgccca ttattcaccc gcttaccggc      60
ctggccgttc cggttggagc tctgcgtacc gcacagagct gcggcatagg ggagtttgcc     120
gacttgccgg ttcttgccga attctgcaaa aaagccggat ttgatcttgt acagcttctt     180
ccggtcaatg acaccggcac agaaagttct ccatacagcg cgctttctgc ctttgccctg     240
cacccgctgt atatcaggct ttccgacctg cctgaagcag cgggtttcga aaagcagatt     300
acagatctga aaagccggtt tgaggacttg cctcgtttca gctatacgga gctgcgccgt     360
gccaaactgg atatcctgcg tgcagtgttt gataaaaaca aggcaaccat catcggcagt     420
gccgaactgg aagcctggat ttcagataac ccctggatca tcgaatatgc ggtttttatg     480
aaccagaaac accgcaactt tgaagccggc tggaaacatt gggaaaagct gcgcaacccc     540
actcataacg aaatacaaaa aacctggcag ggtaaaacct ggcaggctga ccatcaattc     600
tttgcatggc tgcagatgcg gctggaccag cagtttactg ccgccgctac agagtgcaac     660
gccctgggtg tctatcttaa gggcgatata cctataatga tgaacgagga ttccgcagat     720
gcctgggcga atccggaatt cttccgtgac gatcttcggg ccggaagtcc ccctgacggt     780
gaaaaccccc agggacaaaa ctggggcttc cccatttata actgggaaaa ccttgcaaat     840
gacgggtaca gctggtggaa aaaacgtctg aagcacagcg cacggtatta ccatgcctac     900
cgcattgacc atattcttgg gtttttccgg atatgggcta taccctatgg cgaatactcc     960
ggctacctgg gatggccctt gccgcatgaa ccggtaagtg cagcagaact ggcagaacgg    1020
ggcttttcca aggaccgctt gcgctggctt accgaacccc acttgcctac acgggcagcc    1080
gaggaagcga ataactggga ctatctggga acacacggct atctgaatca gatcatgaac    1140
cgtatcggtg aagaagaact atggctgttc aagcccgaga tcacctgcga ggcagatata    1200
cgaaacacaa acctgccgga tgccctgaaa gaggttctgg tacggcagtg gaaaaaccgg    1260
ctgctgcagg ttaccggccg cgacgaaaaa ggacggacaa tctactatcc gctgtggcgt    1320
ttccgtgaca gcactgcatg gcagacgctt accgatggcg agaaacactc cctggaagag    1380
ctgttcgccc aaaaagcggc gcacaatgaa accctgtggc gagaacaggc ggtggaactt    1440
ctgggtgagc tgacgcgatc tacggatatg cttgcctgtg ctgaagatct gggaagtatt    1500
ccccacagtg taccggaagt gctttcaaac ctttcaattt acagtctgcg ggttacccgc    1560
tgggcccgcc aatgggatgc ccccggccag ccctttcaca gactggagga gtatccgctc    1620
atgtcggtag cgaccccatc ggttcatgat tcctctaccc tgcgcggatg gtgggaaacc    1680
gaaggcggcg accgggcctt tatggacgca tggcctccgg aacaggatgc atacgcagga    1740
gcaggccgcc atgagttcga aggcgcctgg ggaccccgcc aggcatcctg ggtactccgt    1800
```

```
aaactctgcg aagcccgttc cgcgctctgt gttttcccca tccaggatat tttggccctg    1860
tcttcagact tttatgcaat gacagcggac gaggaacgca tcaatattcc gggcagtgta    1920
tccggattta actggacata ccggttgcct gcggcaatcg aggatttatc taaaaacagc    1980
caacttataa ccgcaatcca gaccgcgttg caggaccgcc gggcgaggaa ggcacaagga    2040
gcacagcaat ga                                                        2052

<210> 188
<211> 683
<212> PRT
<213> Environmental

<400> 188
Met Tyr Leu Ile Gln Glu Gly His Met Arg Phe Pro Pro Ile Ile His
 1               5                  10                  15
Pro Leu Thr Gly Leu Ala Val Pro Val Gly Ala Leu Arg Thr Ala Gln
            20                  25                  30
Ser Cys Gly Ile Gly Glu Phe Ala Asp Leu Pro Val Leu Ala Glu Phe
        35                  40                  45
Cys Lys Lys Ala Gly Phe Asp Leu Val Gln Leu Leu Pro Val Asn Asp
    50                  55                  60
Thr Gly Thr Glu Ser Ser Pro Tyr Ser Ala Leu Ser Ala Phe Ala Leu
65                  70                  75                  80
His Pro Leu Tyr Ile Arg Leu Ser Asp Leu Pro Glu Ala Ala Gly Phe
                85                  90                  95
Glu Lys Gln Ile Thr Asp Leu Lys Ser Arg Phe Glu Asp Leu Pro Arg
            100                 105                 110
Phe Ser Tyr Thr Glu Leu Arg Arg Ala Lys Leu Asp Ile Leu Arg Ala
        115                 120                 125
Val Phe Asp Lys Asn Lys Ala Thr Ile Ile Gly Ser Ala Glu Leu Glu
    130                 135                 140
Ala Trp Ile Ser Asp Asn Pro Trp Ile Ile Glu Tyr Ala Val Phe Met
145                 150                 155                 160
Asn Gln Lys His Arg Asn Phe Glu Ala Gly Trp Lys His Trp Glu Lys
                165                 170                 175
Leu Arg Asn Pro Thr His Asn Glu Ile Gln Lys Thr Trp Gln Gly Lys
            180                 185                 190
Thr Trp Gln Ala Asp His Gln Phe Phe Ala Trp Leu Gln Met Arg Leu
        195                 200                 205
Asp Gln Gln Phe Thr Ala Ala Ala Thr Glu Cys Asn Ala Leu Gly Val
    210                 215                 220
Tyr Leu Lys Gly Asp Ile Pro Ile Met Met Asn Glu Asp Ser Ala Asp
225                 230                 235                 240
Ala Trp Ala Asn Pro Glu Phe Phe Arg Asp Asp Leu Arg Ala Gly Ser
                245                 250                 255
Pro Pro Asp Gly Glu Asn Pro Gln Gly Gln Asn Trp Gly Phe Pro Ile
            260                 265                 270
Tyr Asn Trp Glu Asn Leu Ala Asn Asp Gly Tyr Ser Trp Trp Lys Lys
        275                 280                 285
Arg Leu Lys His Ser Ala Arg Tyr Tyr His Ala Tyr Arg Ile Asp His
    290                 295                 300
Ile Leu Gly Phe Phe Arg Ile Trp Ala Ile Pro Tyr Gly Glu Tyr Ser
305                 310                 315                 320
Gly Tyr Leu Gly Trp Pro Leu Pro His Glu Pro Val Ser Ala Ala Glu
                325                 330                 335
Leu Ala Glu Arg Gly Phe Ser Lys Asp Arg Leu Arg Trp Leu Thr Glu
            340                 345                 350
Pro His Leu Pro Thr Arg Ala Ala Glu Glu Ala Asn Asn Trp Asp Tyr
```

```
        355                 360                 365
Leu Gly Thr His Gly Tyr Leu Asn Gln Ile Met Asn Arg Ile Gly Glu
    370                 375                 380
Glu Glu Leu Trp Leu Phe Lys Pro Glu Ile Thr Cys Glu Ala Asp Ile
385                 390                 395                 400
Arg Asn Thr Asn Leu Pro Asp Ala Leu Lys Glu Val Leu Val Arg Gln
                405                 410                 415
Trp Lys Asn Arg Leu Leu Gln Val Thr Gly Arg Asp Glu Lys Gly Arg
            420                 425                 430
Thr Ile Tyr Tyr Pro Leu Trp Arg Phe Arg Asp Ser Thr Ala Trp Gln
        435                 440                 445
Thr Leu Thr Asp Gly Glu Lys His Ser Leu Glu Glu Leu Phe Ala Gln
    450                 455                 460
Lys Ala Ala His Asn Glu Thr Leu Trp Arg Glu Gln Ala Val Glu Leu
465                 470                 475                 480
Leu Gly Glu Leu Thr Arg Ser Thr Asp Met Leu Ala Cys Ala Glu Asp
                485                 490                 495
Leu Gly Ser Ile Pro His Ser Val Pro Glu Val Leu Ser Asn Leu Ser
            500                 505                 510
Ile Tyr Ser Leu Arg Val Thr Arg Trp Ala Arg Gln Trp Asp Ala Pro
        515                 520                 525
Gly Gln Pro Phe His Arg Leu Glu Glu Tyr Pro Leu Met Ser Val Ala
    530                 535                 540
Thr Pro Ser Val His Asp Ser Ser Thr Leu Arg Gly Trp Trp Glu Thr
545                 550                 555                 560
Glu Gly Gly Asp Arg Ala Phe Met Asp Ala Trp Pro Pro Glu Gln Asp
                565                 570                 575
Ala Tyr Ala Gly Ala Gly Arg His Glu Phe Glu Gly Ala Trp Gly Pro
            580                 585                 590
Arg Gln Ala Ser Trp Val Leu Arg Lys Leu Cys Glu Ala Arg Ser Ala
        595                 600                 605
Leu Cys Val Phe Pro Ile Gln Asp Ile Leu Ala Leu Ser Ser Asp Phe
    610                 615                 620
Tyr Ala Met Thr Ala Asp Glu Glu Arg Ile Asn Ile Pro Gly Ser Val
625                 630                 635                 640
Ser Gly Phe Asn Trp Thr Tyr Arg Leu Pro Ala Ala Ile Glu Asp Leu
                645                 650                 655
Ser Lys Asn Ser Gln Leu Ile Thr Ala Ile Gln Thr Ala Leu Gln Asp
            660                 665                 670
Arg Arg Ala Arg Lys Ala Gln Gly Ala Gln Gln
        675                 680
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<210> 189
<211> 1596
<212> DNA
<213> Environmental

<400> 189

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atgcaaacga ttgcaaaaaa aggggatgaa acgatgaaag ggaaaaaatg gacagcttta      60
gctctaacac tgccgctggc tgctagctta tcaacaggcg ttcacgccga aaccgtacat     120
aaaggtaaat ctccagctgc agataaaaac ggtgtctttt atgaggtgta tgtaaactct     180
ttttacgatg caaataaaga tggacatggt gatttaaaag gtcttacaca aaaactggac     240
tatttaaatg atggcaattc tcatacaaag aatgatcttc aagtaaacgg gatttggatg     300
atgccgatca acccttctcc tagctatcat aaatatgatg taacggacta ttataacatt     360
gattctcagt acggaaatct gcaagatttt cgcaagctaa tgaaagaagc agataaacga     420
gatgtaaaag ttattatgga cctcgttgtg aatcatacga gcagtgaaca cccttggttt     480
caagctgcgt taaaagataa aaacagcaag tacagagatt actatatttg ggctgataaa     540
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aataccgatt tgaatgaaaa aggatcttgg ggacaacaag tatggcacaa agctccaaac     600
ggagagtatt tttacggaac gttctgggaa ggaatgcctg acttaaatta cgataaccct     660
gaagtaagaa aagaaatgat taacgtcgga aagttttggc taaagcaagg cgttgacggc     720
ttccgcttag atgctgccct tcatatcttt aaaggtcaaa cacctgaagg cgctaagaaa     780
aatattgtgt ggtggaatga atttagagat gcgatgaaaa aagaaaaccc gaacgtatat     840
ctaacgggcg aagtatggga tcagccggaa gtggtagctc cttattatca gtcgcttgat     900
tccctattta actttgattt agcaggaaaa attgtcagct ctgtaaaagc aggaaatgat     960
caaggaatcg ctactgcagc agcggcaaca gatgaactgt tcaaatcata caatccaaat    1020
aaaattgacg gcatttttctt aaccaatcat gaccaaaatc gcgtcatgag tgagttaagc    1080
ggagatgtca ataaagcaaa gtcagctgcc tctatcttac ttacgcttcc tggaaatccg    1140
tatatttatt acggtgaaga aatcggcatg accggtgaaa agcctgatga attaatccgt    1200
gaaccgttcc gctggtacga aggaaacgga cttggacaaa ctagttggga aacacctgta    1260
tacaataaag gcggcaacgg cgtgtctgta gaagcacaaa ccaaacaaaa ggactctttg    1320
ttaaatcatt accgtgaaat gattcgcgtg cgtcagcagc acgaagagtt agtaaaagga    1380
acgcttcaat ctatttcagt agacagtaaa gaagttgttg cttatagccg tacgtataaa    1440
ggcaactcca ttagtgtgta tcataatatt tcaaatcaac ctgtaaaagt atctgtagca    1500
gcgaaaggta aattgatttt tgctagtgaa aaaggtgcta aaaaggtcaa aaatcagctt    1560
gtgattccgg cgaatacaac ggttttagta aaataa                              1596

<210> 190
<211> 531
<212> PRT
<213> Environmental

<400> 190
Met Gln Thr Ile Ala Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys
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Trp Thr Ala Leu Ala Leu Thr Leu Pro Leu Ala Ala Ser Leu Ser Thr
            20                  25                  30
Gly Val His Ala Glu Thr Val His Lys Gly Lys Ser Pro Ala Ala Asp
        35                  40                  45
Lys Asn Gly Val Phe Tyr Glu Val Tyr Val Asn Ser Phe Tyr Asp Ala
    50                  55                  60
Asn Lys Asp Gly His Gly Asp Leu Lys Gly Leu Thr Gln Lys Leu Asp
65                  70                  75                  80
Tyr Leu Asn Asp Gly Asn Ser His Thr Lys Asn Asp Leu Gln Val Asn
                85                  90                  95
Gly Ile Trp Met Met Pro Ile Asn Pro Ser Pro Ser Tyr His Lys Tyr
            100                 105                 110
Asp Val Thr Asp Tyr Tyr Asn Ile Asp Ser Gln Tyr Gly Asn Leu Gln
        115                 120                 125
Asp Phe Arg Lys Leu Met Lys Glu Ala Asp Lys Arg Asp Val Lys Val
    130                 135                 140
Ile Met Asp Leu Val Val Asn His Thr Ser Ser Glu His Pro Trp Phe
145                 150                 155                 160
Gln Ala Ala Leu Lys Asp Lys Asn Ser Lys Tyr Arg Asp Tyr Tyr Ile
                165                 170                 175
Trp Ala Asp Lys Asn Thr Asp Leu Asn Glu Lys Gly Ser Trp Gly Gln
            180                 185                 190
Gln Val Trp His Lys Ala Pro Asn Gly Glu Tyr Phe Tyr Gly Thr Phe
        195                 200                 205
Trp Glu Gly Met Pro Asp Leu Asn Tyr Asp Asn Pro Glu Val Arg Lys
    210                 215                 220
Glu Met Ile Asn Val Gly Lys Phe Trp Leu Lys Gln Gly Val Asp Gly
225                 230                 235                 240
Phe Arg Leu Asp Ala Ala Leu His Ile Phe Lys Gly Gln Thr Pro Glu
                245                 250                 255
```

```
Gly Ala Lys Lys Asn Ile Val Trp Trp Asn Glu Phe Arg Asp Ala Met
            260                 265                 270
Lys Lys Glu Asn Pro Asn Val Tyr Leu Thr Gly Glu Val Trp Asp Gln
        275                 280                 285
Pro Glu Val Val Ala Pro Tyr Tyr Gln Ser Leu Asp Ser Leu Phe Asn
    290                 295                 300
Phe Asp Leu Ala Gly Lys Ile Val Ser Ser Val Lys Ala Gly Asn Asp
305                 310                 315                 320
Gln Gly Ile Ala Thr Ala Ala Ala Ala Thr Asp Glu Leu Phe Lys Ser
                325                 330                 335
Tyr Asn Pro Asn Lys Ile Asp Gly Ile Phe Leu Thr Asn His Asp Gln
            340                 345                 350
Asn Arg Val Met Ser Glu Leu Ser Gly Asp Val Asn Lys Ala Lys Ser
        355                 360                 365
Ala Ala Ser Ile Leu Leu Thr Leu Pro Gly Asn Pro Tyr Ile Tyr Tyr
    370                 375                 380
Gly Glu Glu Ile Gly Met Thr Gly Glu Lys Pro Asp Glu Leu Ile Arg
385                 390                 395                 400
Glu Pro Phe Arg Trp Tyr Glu Gly Asn Gly Leu Gly Gln Thr Ser Trp
                405                 410                 415
Glu Thr Pro Val Tyr Asn Lys Gly Gly Asn Gly Val Ser Val Glu Ala
            420                 425                 430
Gln Thr Lys Gln Lys Asp Ser Leu Leu Asn His Tyr Arg Glu Met Ile
        435                 440                 445
Arg Val Arg Gln Gln His Glu Glu Leu Val Lys Gly Thr Leu Gln Ser
    450                 455                 460
Ile Ser Val Asp Ser Lys Glu Val Val Ala Tyr Ser Arg Thr Tyr Lys
465                 470                 475                 480
Gly Asn Ser Ile Ser Val Tyr His Asn Ile Ser Asn Gln Pro Val Lys
                485                 490                 495
Val Ser Val Ala Ala Lys Gly Lys Leu Ile Phe Ala Ser Glu Lys Gly
            500                 505                 510
Ala Lys Lys Val Lys Asn Gln Leu Val Ile Pro Ala Asn Thr Thr Val
        515                 520                 525
Leu Val Lys
    530
```

<210> 191
<211> 1596
<212> DNA
<213> Environmental

<400> 191

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atgcaaacga ttgcaaaaaa aggggatgaa acgatgaaag ggaaaaaatg gacagcttta      60
gctctaacac tgccgctggc tgctagctta tcaacaggcg ttcacgccga aaccgtacat     120
aaaggtaaat ctccaacagc agataaaaac ggtgtctttt atgaagtgta tgtaaactct     180
ttttacgatg caaataaaga tggacatggt gacttaaaag gtcttacaca aaagttggac     240
tatttaaatg acggcaattc tcatacaaaa aatgatcttc aagtaaacgg gatttggatg     300
atgccagtca acccttctcc tagctatcat aaatatgatg taacggacta ttataacatt     360
gatccgcagt acggaaatct gcaagatttt cgcaagctga tgaaagaagc agacaaacga     420
gacgtaaaag tcattatgga ccttgttgtg aatcatacga gcagtgaaca cccttggttt     480
caagctgcgt taaaagataa aaacagcaag tacagagatt actatatttg ggctgataaa     540
aataccgact tgaatgaaaa aggatcttgg ggacaacaag tatggcataa agctccaaac     600
ggagagtatt tttacggaac gttctgggaa ggaatgcctg acttaaatta cgataaccct     660
gaagtaagaa aagaaatgat taacgtcgga aagttttggc taaagcaagg cgttgacggg     720
ttccgcttag atgctgcgct tcatattttt aaaggtcaaa cagctgaagg cgctaagaaa     780
aatatcctgt ggtggaatga gtttagagat gcgatgaaaa aagaaaatcc gaatgtatat     840
```

```
ctaacgggtg aagtatggga tcagcctgaa gtggtagctc cttattatca atcgcttgat     900
tctttattta attttgattt agcaggaaaa attgtcagct ctgtaaaagc aggaaatgat     960
caaggaatcg ccactgcagc agcagcaaca gatgaactgt tcaaatcata caatccaaac    1020
aaaattgatg gcatattctt aaccaaccat gaccaaaatc gcgtcatgag tgagctgagc    1080
ggcgatgtga gcaaagcaaa atcagctgct tctatcttac ttacgcttcc tggcaacccg    1140
tatatttatt acggtgaaga aatcggcatg accggtgaaa agcctgatga attaatccgt    1200
gaaccgttcc gctggtacga aggaaacgga cttggacaaa ccagttggga aacacctgta    1260
tacaataaag gcggaaacgg tgtgtctgta gaagcacaaa ccaaacaaaa ggattctttg    1320
ttaaatcatt accgtgaaat gattcgcgtg cgtcagcagc atgaagagtt agtaaaagga    1380
acgcttcaat ctatttcagt agacagtaaa gaagttgttg cttatagccg tacgtataaa    1440
ggcaactcca ttagtgtgta tcataatatt tcaaatcaac cggtaaaagt atctgtagca    1500
gcgaaaggta aattgatttt tgctagtgaa aaaggtgcta agaaagtcaa aaatcagctt    1560
gtggttccgg cgaatacaac ggttttaatg aaataa                              1596
```

<210> 192
<211> 531
<212> PRT
<213> Environmental

<400> 192

```
Met Gln Thr Ile Ala Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys
 1               5                  10                  15
Trp Thr Ala Leu Ala Leu Thr Leu Pro Leu Ala Ala Ser Leu Ser Thr
            20                  25                  30
Gly Val His Ala Glu Thr Val His Lys Gly Lys Ser Pro Thr Ala Asp
        35                  40                  45
Lys Asn Gly Val Phe Tyr Glu Val Tyr Val Asn Ser Phe Tyr Asp Ala
    50                  55                  60
Asn Lys Asp Gly His Gly Asp Leu Lys Gly Leu Thr Gln Lys Leu Asp
65                  70                  75                  80
Tyr Leu Asn Asp Gly Asn Ser His Thr Lys Asn Asp Leu Gln Val Asn
                85                  90                  95
Gly Ile Trp Met Met Pro Val Asn Pro Ser Pro Ser Tyr His Lys Tyr
            100                 105                 110
Asp Val Thr Asp Tyr Tyr Asn Ile Asp Pro Gln Tyr Gly Asn Leu Gln
        115                 120                 125
Asp Phe Arg Lys Leu Met Lys Glu Ala Asp Lys Arg Asp Val Lys Val
    130                 135                 140
Ile Met Asp Leu Val Val Asn His Thr Ser Ser Glu His Pro Trp Phe
145                 150                 155                 160
Gln Ala Ala Leu Lys Asp Lys Asn Ser Lys Tyr Arg Asp Tyr Tyr Ile
                165                 170                 175
Trp Ala Asp Lys Asn Thr Asp Leu Asn Glu Lys Gly Ser Trp Gly Gln
            180                 185                 190
Gln Val Trp His Lys Ala Pro Asn Gly Glu Tyr Phe Tyr Gly Thr Phe
        195                 200                 205
Trp Glu Gly Met Pro Asp Leu Asn Tyr Asp Asn Pro Glu Val Arg Lys
    210                 215                 220
Glu Met Ile Asn Val Gly Lys Phe Trp Leu Lys Gln Gly Val Asp Gly
225                 230                 235                 240
Phe Arg Leu Asp Ala Ala Leu His Ile Phe Lys Gly Gln Thr Ala Glu
                245                 250                 255
Gly Ala Lys Lys Asn Ile Leu Trp Trp Asn Glu Phe Arg Asp Ala Met
            260                 265                 270
Lys Lys Glu Asn Pro Asn Val Tyr Leu Thr Gly Glu Val Trp Asp Gln
        275                 280                 285
Pro Glu Val Val Ala Pro Tyr Tyr Gln Ser Leu Asp Ser Leu Phe Asn
```

```
    290                 295                 300
Phe Asp Leu Ala Gly Lys Ile Val Ser Ser Val Lys Ala Gly Asn Asp
305                 310                 315                 320
Gln Gly Ile Ala Thr Ala Ala Ala Ala Thr Asp Glu Leu Phe Lys Ser
                325                 330                 335
Tyr Asn Pro Asn Lys Ile Asp Gly Ile Phe Leu Thr Asn His Asp Gln
            340                 345                 350
Asn Arg Val Met Ser Glu Leu Ser Gly Asp Val Ser Lys Ala Lys Ser
        355                 360                 365
Ala Ala Ser Ile Leu Leu Thr Leu Pro Gly Asn Pro Tyr Ile Tyr Tyr
    370                 375                 380
Gly Glu Glu Ile Gly Met Thr Gly Glu Lys Pro Asp Glu Leu Ile Arg
385                 390                 395                 400
Glu Pro Phe Arg Trp Tyr Glu Gly Asn Gly Leu Gly Gln Thr Ser Trp
                405                 410                 415
Glu Thr Pro Val Tyr Asn Lys Gly Gly Asn Gly Val Ser Val Glu Ala
            420                 425                 430
Gln Thr Lys Gln Lys Asp Ser Leu Leu Asn His Tyr Arg Glu Met Ile
        435                 440                 445
Arg Val Arg Gln Gln His Glu Glu Leu Val Lys Gly Thr Leu Gln Ser
    450                 455                 460
Ile Ser Val Asp Ser Lys Glu Val Val Ala Tyr Ser Arg Thr Tyr Lys
465                 470                 475                 480
Gly Asn Ser Ile Ser Val Tyr His Asn Ile Ser Asn Gln Pro Val Lys
                485                 490                 495
Val Ser Val Ala Ala Lys Gly Lys Leu Ile Phe Ala Ser Glu Lys Gly
            500                 505                 510
Ala Lys Lys Val Lys Asn Gln Leu Val Val Pro Ala Asn Thr Thr Val
        515                 520                 525
Leu Met Lys
    530
```

<210> 193
<211> 1962
<212> DNA
<213> Environmental

<400> 193

```
atgaaattca aaaagagttt atctgccggg ctccttttgt tcggaggtct gagcggtgtg      60
acaccatccg tcgctgcgga ggtgccacga accgcatttg tccatttatt cgaatggagt     120
tggccggata ttgccaccga atgcgaaacc tttcttggcc ctaaggggtt ctctgcggtt     180
caggtgtctc cgccgcaaaa aagcgtcagc aatgctgcct ggtgggcgcg ctaccaacct     240
gttagttact cttttgaagg gcgcagtgga acccgggctc aatttgcgga tatggtccag     300
cgttgtaaag cggtgggggt cgatatttat ctggatgcgg tgatcaacca tatggcagca     360
caagatcgct attttccaga agtaccttac agcagtaatg attttcacag ttgcacgggc     420
gatatcgatt attccaaccg ctggtcgatt caaaattgcg atctggttgg gctgaacgat     480
ctcaaaaccg agtcagaata cgttcggcag aaaattgcag actatatgaa cgatgcgctc     540
agtctgggcg tggcggggtt tcggattgat gccgccaagc atatcccggc cggcgacatc     600
gcggcgatca agagcaagct caacggcagc ccgtatatct atcaggaggt tatcggggcg     660
gcaggggagc cggtacaaac cagcgagtac acgtatattg gagacgtgac ggaatttaac     720
ttcgcccgga ccatcgggcc taaatttaag caaggtaata ttaaagacct gcaggggatt     780
ggttcgtgga gcggctggct gagcagcgac gatgcggtga cctttgtgac caaccatgac     840
gaagaacgcc ataaccctgg ccaggttctc agccatcagg actttggcaa tctgtatttc     900
ctcggtaacg tgtttactct ggcgtatcct tacggctacc caaaagtgat gtcggggtac     960
tacttcagta attttgatgc cgggccacca tcgacagggg tacattctgg taatgcgtgt    1020
ggctttgatg gcggtgattg ggtctgcgaa cacaaatggc gtggtgtagc caacatggtg    1080
gcgtttcgca accacacagc agcccagtgg caggtcactg actggtggga cgatggttac    1140
```

```
aatcaggtgg cgtttggtcg tggcgggctg ggctttgtgg tgatcaatcg agatgacaat    1200
aaaggcatca atcagagttt ccagacggga atgcccgctg gcgagtattg tgacatcatt    1260
gccggtgatt tcgacaccca gagcggtcat tgcagcgcta cgacgatcac cgtcgacagt    1320
caggggtatg cacattttac tgtcggtagt catcaggccg ctgcgattca cattggcgcg    1380
aaactcggct ccgtgtgcca ggactgtggc ggcacggccg cagagacaaa agtctgcttt    1440
gacaatgcac aaaactttag ccaaccgtat ttgcattact ggaatgtcaa tgcggatcag    1500
gccgtagcga atgcaacctg gccgggcgtc gcgatgacgg ctgaaaatgg cggttactgc    1560
tacgattttg gtgtcggtct caattcactt caggtaattt tcagcgataa cggcgccagc    1620
caaaccgctg atctgaccgc cagcagtccg acgttgtgtt accagaacgg aacgtggcgt    1680
gacagtgact tctgtcagag tagcaatgtg ggcaacgaga gttggtattt ccgtggaacc    1740
tcaaacggtt ggggcgtgag cgcactcact tatgaggctg cgacaggcct gtacactacg    1800
gtgcagagct ttaacgggga ggagtcgccc gcacgcttta aaattgatga tggcaactgg    1860
agtgagtcgt atccaagtgc tgattatcaa gtcggtgatt atgccaccta cacgatcacg    1920
tttgacagcc agacgaaggc catcaccgtg acttcgcagt aa                       1962
```

<210> 194
<211> 653
<212> PRT
<213> Environmental

<400> 194

```
Met Lys Phe Lys Lys Ser Leu Ser Ala Gly Leu Leu Leu Phe Gly Gly
 1               5                  10                  15
Leu Ser Gly Val Thr Pro Ser Val Ala Ala Glu Val Pro Arg Thr Ala
            20                  25                  30
Phe Val His Leu Phe Glu Trp Ser Trp Pro Asp Ile Ala Thr Glu Cys
        35                  40                  45
Glu Thr Phe Leu Gly Pro Lys Gly Phe Ser Ala Val Gln Val Ser Pro
    50                  55                  60
Pro Gln Lys Ser Val Ser Asn Ala Ala Trp Trp Ala Arg Tyr Gln Pro
65                  70                  75                  80
Val Ser Tyr Ser Phe Glu Gly Arg Ser Gly Thr Arg Ala Gln Phe Ala
                85                  90                  95
Asp Met Val Gln Arg Cys Lys Ala Val Gly Val Asp Ile Tyr Leu Asp
            100                 105                 110
Ala Val Ile Asn His Met Ala Ala Gln Asp Arg Tyr Phe Pro Glu Val
        115                 120                 125
Pro Tyr Ser Ser Asn Asp Phe His Ser Cys Thr Gly Asp Ile Asp Tyr
    130                 135                 140
Ser Asn Arg Trp Ser Ile Gln Asn Cys Asp Leu Val Gly Leu Asn Asp
145                 150                 155                 160
Leu Lys Thr Glu Ser Glu Tyr Val Arg Gln Lys Ile Ala Asp Tyr Met
                165                 170                 175
Asn Asp Ala Leu Ser Leu Gly Val Ala Gly Phe Arg Ile Asp Ala Ala
            180                 185                 190
Lys His Ile Pro Ala Gly Asp Ile Ala Ala Ile Lys Ser Lys Leu Asn
        195                 200                 205
Gly Ser Pro Tyr Ile Tyr Gln Glu Val Ile Gly Ala Ala Gly Glu Pro
    210                 215                 220
Val Gln Thr Ser Glu Tyr Thr Tyr Ile Gly Asp Val Thr Glu Phe Asn
225                 230                 235                 240
Phe Ala Arg Thr Ile Gly Pro Lys Phe Lys Gln Gly Asn Ile Lys Asp
                245                 250                 255
Leu Gln Gly Ile Gly Ser Trp Ser Gly Trp Leu Ser Ser Asp Asp Ala
            260                 265                 270
Val Thr Phe Val Thr Asn His Asp Glu Glu Arg His Asn Pro Gly Gln
        275                 280                 285
```

```
Val Leu Ser His Gln Asp Phe Gly Asn Leu Tyr Phe Leu Gly Asn Val
    290                 295                 300
Phe Thr Leu Ala Tyr Pro Tyr Gly Tyr Pro Lys Val Met Ser Gly Tyr
305                 310                 315                 320
Tyr Phe Ser Asn Phe Asp Ala Gly Pro Pro Ser Thr Gly Val His Ser
                325                 330                 335
Gly Asn Ala Cys Gly Phe Asp Gly Gly Asp Trp Val Cys Glu His Lys
            340                 345                 350
Trp Arg Gly Val Ala Asn Met Val Ala Phe Arg Asn His Thr Ala Ala
        355                 360                 365
Gln Trp Gln Val Thr Asp Trp Trp Asp Asp Gly Tyr Asn Gln Val Ala
    370                 375                 380
Phe Gly Arg Gly Gly Leu Gly Phe Val Val Ile Asn Arg Asp Asp Asn
385                 390                 395                 400
Lys Gly Ile Asn Gln Ser Phe Gln Thr Gly Met Pro Ala Gly Glu Tyr
                405                 410                 415
Cys Asp Ile Ile Ala Gly Asp Phe Asp Thr Gln Ser Gly His Cys Ser
            420                 425                 430
Ala Thr Thr Ile Thr Val Asp Ser Gln Gly Tyr Ala His Phe Thr Val
        435                 440                 445
Gly Ser His Gln Ala Ala Ala Ile His Ile Gly Ala Lys Leu Gly Ser
    450                 455                 460
Val Cys Gln Asp Cys Gly Gly Thr Ala Ala Glu Thr Lys Val Cys Phe
465                 470                 475                 480
Asp Asn Ala Gln Asn Phe Ser Gln Pro Tyr Leu His Tyr Trp Asn Val
                485                 490                 495
Asn Ala Asp Gln Ala Val Ala Asn Ala Thr Trp Pro Gly Val Ala Met
            500                 505                 510
Thr Ala Glu Asn Gly Gly Tyr Cys Tyr Asp Phe Gly Val Gly Leu Asn
        515                 520                 525
Ser Leu Gln Val Ile Phe Ser Asp Asn Gly Ala Ser Gln Thr Ala Asp
    530                 535                 540
Leu Thr Ala Ser Ser Pro Thr Leu Cys Tyr Gln Asn Gly Thr Trp Arg
545                 550                 555                 560
Asp Ser Asp Phe Cys Gln Ser Ser Asn Val Gly Asn Glu Ser Trp Tyr
                565                 570                 575
Phe Arg Gly Thr Ser Asn Gly Trp Gly Val Ser Ala Leu Thr Tyr Glu
            580                 585                 590
Ala Ala Thr Gly Leu Tyr Thr Thr Val Gln Ser Phe Asn Gly Glu Glu
        595                 600                 605
Ser Pro Ala Arg Phe Lys Ile Asp Asp Gly Asn Trp Ser Glu Ser Tyr
    610                 615                 620
Pro Ser Ala Asp Tyr Gln Val Gly Asp Tyr Ala Thr Tyr Thr Ile Thr
625                 630                 635                 640
Phe Asp Ser Gln Thr Lys Ala Ile Thr Val Thr Ser Gln
                645                 650
```

<210> 195
<211> 2790
<212> DNA
<213> Environmental

<400> 195

```
atgctgacag accgtttctt tgatggcgat acatcaaaca acgaccctta caaccagaac      60
tacgatgcta aaaacgaccg gggaacttat cagggcggcg attttaaagg aatcacgcaa     120
aaattggatt atctcgataa gctaggcgtg aacacaatct ggatcagccc gatcgtggaa     180
aatatcaagc atgatgtccg ttatgacaac tctgaagggc attcatacta tgcttaccac     240
```

```
ggctactggg caagcaactt cggtgcgtta aacccacact tcggtacaat ggaagatttc     300
catacactga ttgacgctgc ccatgaaaaa ggcatcaaga tcatggttga cgtagtatta     360
aaccacactg gttatggctt aaaagatatc aacggagaag tttccaatcc tccagccggt     420
tacccaactg acgcagaacg cagcacatat agcagcctgc ttcgccaggg ttcaaatgtc     480
ggctctgatg aggttgttgg cgaattagct ggcctacctg acttaaaaac agaagacccc     540
gcagtccgcc agacaatcat cgactggcaa acagactgga tcacgaaagc tactacagct     600
aaaggaaaca caattgacta cttccgtgtc gacactgtga agcacgttga agacgcaaca     660
tggatggcat tcaaaaatga cctcactgaa aaaatgccga cacacaaaat gatcggggaa     720
gcttggggag caagtgccaa taaccaactt ggataccttg aaacaggtat gatggactca     780
ctgcttgact tcgacttcaa aggcattgcg cacgatttcg tgaacggcaa gcttaaggca     840
gcaaacgatg ccctgactgc ccgcaacggt aaaattgaca acacagctac tttaggttca     900
ttccttggaa gccatgacga agatggtttc ctatttaaag aaggaaatga caaaggcaag     960
cttaaggttg ctgcttccct gcaagcaaca tcaaaaggcc agccggtcat ctattatggt    1020
gaagagcttg gtcaaagtgg agcaaacaac tatccgcaat acgataaccg ttatgacctg    1080
gcatgggaca aagttgaaaa caacgacgtc cttgagcact acactaaggt cctgaacttc    1140
agaagcgctc attcagaagt gttcgctaaa ggtgaacgcg caacaattgg cggttctgac    1200
gctgataaat tcttactttt tgctcgtaaa aatggaaacg aagctgctta cgtcggcttg    1260
aacgttgctg acacagcaaa agacgtaaca ctgactgttt ctgcaggtgc agtcgtaact    1320
gaccactatg cagataaaac ttatactgct tcagaagctg gagaaatcac attgacgatc    1380
ccggcaaaag ctgatggcgg tactgtttta ctaacggttg aaggcggaga aatcacagct    1440
gctaaagcgg caagcgaagg cgacggcaca gttgagccag tccctgcgaa ccacatccgc    1500
attcactaca accgtacaga caacaactat gaaaactacg gtgcatggct gtggaacgat    1560
gtagcctccc cttctgccaa ctggccgact ggcgctacaa tgtttgaaaa aacagacagc    1620
tacggtgcat acatcgacgt accacttaaa gagggcgcta agaacatcgg cttcctcgtt    1680
atggatgtaa caaaaggtga tcagggtaaa gacggcggcg acaaaggttt tacgatctca    1740
tcacctgaaa tgaacgaaat ttggatcaag caaggttctg acaaggtgta cacttacgag    1800
ccagttgatc ttccggcgaa cactgtccgc gtccactatg tacgtgacaa cgcagactac    1860
gaaaacttcg gtatctggaa ctggggcgat gtaacagcac cttccgaaaa ctggcctaca    1920
ggcgcagcga aattcgatgg tacagaccgt tacggtgcgt atgtcgacat tacgctaaaa    1980
gaaggcgcaa agaacattgg aatgattgct cttaacactg caaatggaga gaaagacggc    2040
ggagataaat ccttcaacct tctggataaa tataatcgca tttggattaa acaaggtgat    2100
gacaatgtct acgtttctcc atactgggag caggcaacag gaatcaccaa tgcagaggta    2160
atctctgaag atacgattct attaggcttc acaatgactg acggcttaac acctgaatct    2220
ttaaaaggag gtcttgtaat taaagattca actggtgctg aagttgccat cgaaagtgct    2280
gaaatcacaa gcgcaacctc tgtaaaagta aaagcaacat tcgatttaga aaagcttcca    2340
ttatccatca catacgcagg cagaacagtt tcagcttcaa ctggctggag aatgcttgat    2400
gaaatgtacg cttatgatgg aaacgacctt ggtgcgactt acaaggacgg agcagcgacg    2460
cttaaattat gggctccgaa agcgagcaag gtaaccgcta acttctttga taaaaataat    2520
gccgctgaaa aaatcggcag cgtcgagtta acgaagggtg aaaaaggagt ctggtcagct    2580
atggttgctc ctggcgacct gaacgtaacc gatcttgaag gttattttta ccagtatgat    2640
gtaacaaatg acggtataac tcgccaggtg ttagatcctt atgcaaaatc aatggcagcc    2700
tttactgtga atacagaagg caatgctggt cctgacgggg acactgttgg caaggcggca    2760
attcaaaaag cttctcgaga gtacttctag                                     2790
```

<210> 196
<211> 929
<212> PRT
<213> Environmental

<400> 196

```
Met Leu Thr Asp Arg Phe Phe Asp Gly Asp Thr Ser Asn Asn Asp Pro
 1               5                  10                  15
Tyr Asn Gln Asn Tyr Asp Ala Lys Asn Asp Arg Gly Thr Tyr Gln Gly
            20                  25                  30
Gly Asp Phe Lys Gly Ile Thr Gln Lys Leu Asp Tyr Leu Asp Lys Leu
        35                  40                  45
Gly Val Asn Thr Ile Trp Ile Ser Pro Ile Val Glu Asn Ile Lys His
```

```
     50                  55                  60
Asp Val Arg Tyr Asp Asn Ser Glu Gly His Ser Tyr Tyr Ala Tyr His
65                  70                  75                  80
Gly Tyr Trp Ala Ser Asn Phe Gly Ala Leu Asn Pro His Phe Gly Thr
                85                  90                  95
Met Glu Asp Phe His Thr Leu Ile Asp Ala Ala His Glu Lys Gly Ile
            100                 105                 110
Lys Ile Met Val Asp Val Val Leu Asn His Thr Gly Tyr Gly Leu Lys
        115                 120                 125
Asp Ile Asn Gly Glu Val Ser Asn Pro Pro Ala Gly Tyr Pro Thr Asp
    130                 135                 140
Ala Glu Arg Ser Thr Tyr Ser Ser Leu Leu Arg Gln Gly Ser Asn Val
145                 150                 155                 160
Gly Ser Asp Glu Val Val Gly Glu Leu Ala Gly Leu Pro Asp Leu Lys
                165                 170                 175
Thr Glu Asp Pro Ala Val Arg Gln Thr Ile Ile Asp Trp Gln Thr Asp
            180                 185                 190
Trp Ile Thr Lys Ala Thr Thr Ala Lys Gly Asn Thr Ile Asp Tyr Phe
        195                 200                 205
Arg Val Asp Thr Val Lys His Val Glu Asp Ala Thr Trp Met Ala Phe
    210                 215                 220
Lys Asn Asp Leu Thr Glu Lys Met Pro Thr His Lys Met Ile Gly Glu
225                 230                 235                 240
Ala Trp Gly Ala Ser Ala Asn Asn Gln Leu Gly Tyr Leu Glu Thr Gly
                245                 250                 255
Met Met Asp Ser Leu Leu Asp Phe Asp Phe Lys Gly Ile Ala His Asp
            260                 265                 270
Phe Val Asn Gly Lys Leu Lys Ala Ala Asn Asp Ala Leu Thr Ala Arg
        275                 280                 285
Asn Gly Lys Ile Asp Asn Thr Ala Thr Leu Gly Ser Phe Leu Gly Ser
    290                 295                 300
His Asp Glu Asp Gly Phe Leu Phe Lys Glu Gly Asn Asp Lys Gly Lys
305                 310                 315                 320
Leu Lys Val Ala Ala Ser Leu Gln Ala Thr Ser Lys Gly Gln Pro Val
                325                 330                 335
Ile Tyr Tyr Gly Glu Glu Leu Gly Gln Ser Gly Ala Asn Asn Tyr Pro
            340                 345                 350
Gln Tyr Asp Asn Arg Tyr Asp Leu Ala Trp Asp Lys Val Glu Asn Asn
        355                 360                 365
Asp Val Leu Glu His Tyr Thr Lys Val Leu Asn Phe Arg Ser Ala His
    370                 375                 380
Ser Glu Val Phe Ala Lys Gly Glu Arg Ala Thr Ile Gly Gly Ser Asp
385                 390                 395                 400
Ala Asp Lys Phe Leu Leu Phe Ala Arg Lys Asn Gly Asn Glu Ala Ala
                405                 410                 415
Tyr Val Gly Leu Asn Val Ala Asp Thr Ala Lys Asp Val Thr Leu Thr
            420                 425                 430
Val Ser Ala Gly Ala Val Val Thr Asp His Tyr Ala Asp Lys Thr Tyr
        435                 440                 445
Thr Ala Ser Glu Ala Gly Glu Ile Thr Leu Thr Ile Pro Ala Lys Ala
    450                 455                 460
Asp Gly Gly Thr Val Leu Leu Thr Val Glu Gly Gly Glu Ile Thr Ala
465                 470                 475                 480
Ala Lys Ala Ala Ser Glu Gly Asp Gly Thr Val Glu Pro Val Pro Ala
                485                 490                 495
Asn His Ile Arg Ile His Tyr Asn Arg Thr Asp Asn Asn Tyr Glu Asn
            500                 505                 510
```

```
Tyr Gly Ala Trp Leu Trp Asn Asp Val Ala Ser Pro Ser Ala Asn Trp
        515                 520                 525
Pro Thr Gly Ala Thr Met Phe Glu Lys Thr Asp Ser Tyr Gly Ala Tyr
    530                 535                 540
Ile Asp Val Pro Leu Lys Glu Gly Ala Lys Asn Ile Gly Phe Leu Val
545                 550                 555                 560
Met Asp Val Thr Lys Gly Asp Gln Gly Lys Asp Gly Gly Asp Lys Gly
                565                 570                 575
Phe Thr Ile Ser Ser Pro Glu Met Asn Glu Ile Trp Ile Lys Gln Gly
            580                 585                 590
Ser Asp Lys Val Tyr Thr Tyr Glu Pro Val Asp Leu Pro Ala Asn Thr
        595                 600                 605
Val Arg Val His Tyr Val Arg Asp Asn Ala Asp Tyr Glu Asn Phe Gly
    610                 615                 620
Ile Trp Asn Trp Gly Asp Val Thr Ala Pro Ser Glu Asn Trp Pro Thr
625                 630                 635                 640
Gly Ala Ala Lys Phe Asp Gly Thr Asp Arg Tyr Gly Ala Tyr Val Asp
                645                 650                 655
Ile Thr Leu Lys Glu Gly Ala Lys Asn Ile Gly Met Ile Ala Leu Asn
            660                 665                 670
Thr Ala Asn Gly Glu Lys Asp Gly Gly Asp Lys Ser Phe Asn Leu Leu
        675                 680                 685
Asp Lys Tyr Asn Arg Ile Trp Ile Lys Gln Gly Asp Asp Asn Val Tyr
    690                 695                 700
Val Ser Pro Tyr Trp Glu Gln Ala Thr Gly Ile Thr Asn Ala Glu Val
705                 710                 715                 720
Ile Ser Glu Asp Thr Ile Leu Leu Gly Phe Thr Met Thr Asp Gly Leu
                725                 730                 735
Thr Pro Glu Ser Leu Lys Gly Gly Leu Val Ile Lys Asp Ser Thr Gly
            740                 745                 750
Ala Glu Val Ala Ile Glu Ser Ala Glu Ile Thr Ser Ala Thr Ser Val
        755                 760                 765
Lys Val Lys Ala Thr Phe Asp Leu Glu Lys Leu Pro Leu Ser Ile Thr
    770                 775                 780
Tyr Ala Gly Arg Thr Val Ser Ala Ser Thr Gly Trp Arg Met Leu Asp
785                 790                 795                 800
Glu Met Tyr Ala Tyr Asp Gly Asn Asp Leu Gly Ala Thr Tyr Lys Asp
                805                 810                 815
Gly Ala Ala Thr Leu Lys Leu Trp Ala Pro Lys Ala Ser Lys Val Thr
            820                 825                 830
Ala Asn Phe Phe Asp Lys Asn Asn Ala Ala Glu Lys Ile Gly Ser Val
        835                 840                 845
Glu Leu Thr Lys Gly Glu Lys Gly Val Trp Ser Ala Met Val Ala Pro
    850                 855                 860
Gly Asp Leu Asn Val Thr Asp Leu Glu Gly Tyr Phe Tyr Gln Tyr Asp
865                 870                 875                 880
Val Thr Asn Asp Gly Ile Thr Arg Gln Val Leu Asp Pro Tyr Ala Lys
                885                 890                 895
Ser Met Ala Ala Phe Thr Val Asn Thr Glu Gly Asn Ala Gly Pro Asp
            900                 905                 910
Gly Asp Thr Val Gly Lys Ala Ala Ile Gln Lys Ala Ser Arg Glu Tyr
        915                 920                 925
Phe
```

<210> 197
<211> 1401

<212> DNA
<213> Environmental

<400> 197
atgaaaccgt caaaattcgt ttttctctct gctgccatcg cttgcagcct ctccagtacc 60
gccaatgctg acgccatttt gcatgcattt aactggaagt actccgacgt cacgcaaaac 120
gcctcgcaaa tcgcggcggc gggttataaa aaagtgctga tttcgccagc actgaaatcg 180
agtggcaatg aatggtgggc acgttatcaa ccgcaagatc tgcgcgtgat cgattcccca 240
cttggcaaca aaagtgactt aaaatccatg attgatgctc tgaaggcggt cggcgttgat 300
gtgtatgccg atgtggtgct taaccatatg gccaatgaaa catggaagcg tgaagactta 360
aattaccctg gcagtgaagt gctgcaacaa tacgcagcta acaccagtta ttatgcggac 420
caaacgcttt ttggcaattt aacggaaaac ctattctctg gctttgactt ccacccagaa 480
ggctgtatta gcgattggaa tgatgccggc aatgttcagt actggcgtct ttgtggcggt 540
gctggtgacc gagggctgcc agacttagat ccgaacaact gggtggtgtc acagcaacgt 600
ttgtatttga atgcgctaaa aggtttaggt gtgaaaggct tccgcattga tgcggttaaa 660
cacatgagcc aatatcaaat cgaccagatt ttcactgcag agattaccgc cggaatgcac 720
gtgtttggtg aagtgatcac cagtggtggc aaaggcgact ccagctatga gaacttctta 780
gcgccttatc tcaacgccac caaccattcg gcttacgatt tcccactgtt tgcctctatt 840
cgcaacgcct tctcctacag cggtggcatg aacatgcttc atgatccaca agcctatggc 900
caagggcttg aaaacgcacg ttcaattacc tttaccatca cgcacgacat cccaacgaac 960
gacggtttcc gttatcaaat catggatccg aaagatgaag agctggctta cgcttatatc 1020
ctcggtaaag atggcggcac acctctgatt tacagcgaca acttacctga taacgaagat 1080
cgtgataatc gccgttggga aggtgtttgg aaccgtgacc tgatgaagaa catgttgcgc 1140
ttccataacc aaatgcaagg gcaagagatg acgatgctgt acagcgacca atgtctactg 1200
atgtttaagc gcggtaaaca aggggtggtc ggcattaata aatgcggtga agagcgttct 1260
cataccgttg acacctatca gcatgagttc aactggtatc agccttacac agatacactc 1320
actggcgtga ctgaaaccgt gagttcgcgt taccacacct tccgaattcc agctcgcagc 1380
gcgcgcatgt acatgctcta a 1401

<210> 198
<211> 466
<212> PRT
<213> Environmental

<400> 198
Met Lys Pro Ser Lys Phe Val Phe Leu Ser Ala Ala Ile Ala Cys Ser
1 5 10 15
Leu Ser Ser Thr Ala Asn Ala Asp Ala Ile Leu His Ala Phe Asn Trp
20 25 30
Lys Tyr Ser Asp Val Thr Gln Asn Ala Ser Gln Ile Ala Ala Ala Gly
35 40 45
Tyr Lys Lys Val Leu Ile Ser Pro Ala Leu Lys Ser Ser Gly Asn Glu
50 55 60
Trp Trp Ala Arg Tyr Gln Pro Gln Asp Leu Arg Val Ile Asp Ser Pro
65 70 75 80
Leu Gly Asn Lys Ser Asp Leu Lys Ser Met Ile Asp Ala Leu Lys Ala
85 90 95
Val Gly Val Asp Val Tyr Ala Asp Val Val Leu Asn His Met Ala Asn
100 105 110
Glu Thr Trp Lys Arg Glu Asp Leu Asn Tyr Pro Gly Ser Glu Val Leu
115 120 125
Gln Gln Tyr Ala Ala Asn Thr Ser Tyr Tyr Ala Asp Gln Thr Leu Phe
130 135 140
Gly Asn Leu Thr Glu Asn Leu Phe Ser Gly Phe Asp Phe His Pro Glu
145 150 155 160
Gly Cys Ile Ser Asp Trp Asn Asp Ala Gly Asn Val Gln Tyr Trp Arg
165 170 175

```
Leu Cys Gly Gly Ala Gly Asp Arg Gly Leu Pro Asp Leu Asp Pro Asn
            180                 185                 190
Asn Trp Val Val Ser Gln Gln Arg Leu Tyr Leu Asn Ala Leu Lys Gly
        195                 200                 205
Leu Gly Val Lys Gly Phe Arg Ile Asp Ala Val Lys His Met Ser Gln
    210                 215                 220
Tyr Gln Ile Asp Gln Ile Phe Thr Ala Glu Ile Thr Ala Gly Met His
225                 230                 235                 240
Val Phe Gly Glu Val Ile Thr Ser Gly Gly Lys Gly Asp Ser Ser Tyr
                245                 250                 255
Glu Asn Phe Leu Ala Pro Tyr Leu Asn Ala Thr Asn His Ser Ala Tyr
            260                 265                 270
Asp Phe Pro Leu Phe Ala Ser Ile Arg Asn Ala Phe Ser Tyr Ser Gly
        275                 280                 285
Gly Met Asn Met Leu His Asp Pro Gln Ala Tyr Gly Gln Gly Leu Glu
    290                 295                 300
Asn Ala Arg Ser Ile Thr Phe Thr Ile Thr His Asp Ile Pro Thr Asn
305                 310                 315                 320
Asp Gly Phe Arg Tyr Gln Ile Met Asp Pro Lys Asp Glu Glu Leu Ala
                325                 330                 335
Tyr Ala Tyr Ile Leu Gly Lys Asp Gly Gly Thr Pro Leu Ile Tyr Ser
            340                 345                 350
Asp Asn Leu Pro Asp Asn Glu Asp Arg Asp Asn Arg Arg Trp Glu Gly
        355                 360                 365
Val Trp Asn Arg Asp Leu Met Lys Asn Met Leu Arg Phe His Asn Gln
    370                 375                 380
Met Gln Gly Gln Glu Met Thr Met Leu Tyr Ser Asp Gln Cys Leu Leu
385                 390                 395                 400
Met Phe Lys Arg Gly Lys Gln Gly Val Val Gly Ile Asn Lys Cys Gly
                405                 410                 415
Glu Glu Arg Ser His Thr Val Asp Thr Tyr Gln His Glu Phe Asn Trp
            420                 425                 430
Tyr Gln Pro Tyr Thr Asp Thr Leu Thr Gly Val Thr Glu Thr Val Ser
        435                 440                 445
Ser Arg Tyr His Thr Phe Arg Ile Pro Ala Arg Ser Ala Arg Met Tyr
    450                 455                 460
Met Leu
465
```

<210> 199
<211> 399
<212> DNA
<213> Environmental

<400> 199

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gtgagtttga ccaaaaaggc tcagtacgaa ccaaatacgg caccaaggct cagtacatct      60
ctgcaatcaa tgccgcgcac aacaacaata tccaaattta cggcgatgtt gtgtttaacc     120
accgaggtgg tgctgatggg aagtcgtggg tcgataccaa gcgcgttgat tgggacaacc     180
gcaatattga actgggcgac aaatggattg aagcttgggt tgagtttaat tttcctggcc     240
gcaacgacaa atactcgaac ttccattgga cttggtatca ctttgacggt gttgactggg     300
atgacgccgg caaagaaaaa gcgatcttta aattcaaagg cgaaggaaaa gcatgggatt     360
gggaagtcag ctctgaaaaa ggcaattacg actacctaa                            399
```

<210> 200
<211> 132
<212> PRT
<213> Environmental

<400> 200
Val Ser Leu Thr Lys Lys Ala Gln Tyr Glu Pro Asn Thr Ala Pro Arg
1 5 10 15
Leu Ser Thr Ser Leu Gln Ser Met Pro Arg Thr Thr Thr Ile Ser Lys
20 25 30
Phe Thr Ala Met Leu Cys Leu Thr Thr Glu Val Val Leu Met Gly Ser
35 40 45
Arg Gly Ser Ile Pro Ser Ala Leu Ile Gly Thr Thr Ala Ile Leu Asn
50 55 60
Trp Ala Thr Asn Gly Leu Lys Leu Gly Leu Ser Leu Ile Phe Leu Ala
65 70 75 80
Ala Thr Thr Asn Thr Arg Thr Ser Ile Gly Leu Gly Ile Thr Leu Thr
85 90 95
Val Leu Thr Gly Met Thr Pro Ala Lys Lys Lys Arg Ser Leu Asn Ser
100 105 110
Lys Ala Lys Glu Lys His Gly Ile Gly Lys Ser Ala Leu Lys Lys Ala
115 120 125
Ile Thr Thr Thr
130

<210> 201
<211> 1911
<212> DNA
<213> Environmental

<400> 201
atgacagcca aggctgatga cttacgcatt taccagatca tggtggaaag ctttgtggat 60
ggcgataaac aggtcggcca tggcaccggc tacggtacca gccatcacaa aggcgatctg 120
caagggatca ttgactcgct ggattacatt caatcgctgg gcgtcaatgc catttggcta 180
acgccgattt ttgaatctat tccggtggag ggacaagacc attgggcgga caggcttgat 240
gctacaggct actttgccag tgactatttc aagatagacc ctcgctttgg cacgttagaa 300
caagcccgtg agctggtgga aaaggcacac gcgaaaggct tgtatgtctt ctttgatgga 360
gtatttggtc accataaagg caatgtggtg ccatcaccac aaggtagact gcctgtcggt 420
gaaaataacc cggtcagcta cccagagagc ctggcgtttt acgaagaagt cgccagttac 480
tgggtgaaag agttaaagat tgatggctgg cgtctggatc aagcctatca agtgccgacc 540
gatgcatgga aagcgatccg tcagagcgtt gatgaagcgt cacagtccgt aacttatgtg 600
aataacaaag gggaaaccgt ccatcctttg ggttacatgg tggctgaaat ttggaataac 660
gaacgttaca tcacagaaac cggttacggc aaagaaggcg atccggcgtt gtgctcggct 720
tttgattttc cgatgcgttt ccgagtggtc gaaacctttg cggttaacga aagtggtgtc 780
agccgaaaag gcggcgaatg gttgaatgac ggcatgtcac tgcacagtca gtatccggat 840
catgccaagc ctaatttaat gttgggcaac catgatgtgg tgcgctttgg ggatctgctg 900
caacgtggcg gtattgcgtc accagaacaa ccgcaatact ggcagcgtca taaagcggcg 960
atgtctttct tagcagcgta taccggccca attaccttgt attacggtga agaaattggc 1020
gatcaggttg acggctttgc taaaaaaatc aaagaagatt gtgccgttat tggtttgtgt 1080
gatgaccacg tggcgcgcac cagtgcgaag attgatggcg tgacggcgtc actgaatgca 1140
cagcagtctg aactcaaagt atatgtctct tcattgatga cattacgtca gcaacatcct 1200
gcgttatcac aaggggaacg tactaatgtg atggcgacag agacagtata cgtagaccat 1260
aaacaggcag acaatgaagc cctgttgtac atggtgagta cgactgataa cgcggagtca 1320
gtcaccttga agggcaaagc gattggttca caaggtgtgc tgattgattt gttaacgaac 1380
gagcgtttta tgcccaataa tggggagtat gccattccat taacgggctt tggcgcacga 1440
ttcctcaaga ttgacactcc gacagcggcg ggtgtgatgg cgcaatctgc tgcctcggta 1500
tcgctagtag gtgaagggat catggcccaa tgtgataccc caaccgttga aggcaccggt 1560
ccggtagcag aaaccttgta cgtggttggc gattttgccg atgctggttg gaagcaaaag 1620
ccgcagcgcg cgtatcaata caaaggcaag cacaatggca gcaacttgta tcaagtggtt 1680
gtcgatgaaa aagcgggcgc ctacaagatg caatacgcca cgaaagattg gagcccacag 1740
tttactgcag acggtatggc attgaagccg ggtaccgcaa agtcgctcat agcgggtggc 1800

tacggtaaag acaccgccgt gacgttgccg gaatccggta agtatgtgtg gagcttaaca 1860
ttcagtgatc ttggcgagcc ggagcaaatc atggtgtcta agtgtcagta a 1911

<210> 202
<211> 630
<212> PRT
<213> Environmental

<400> 202
Met Thr Ala Lys Ala Asp Asp Leu Arg Ile Tyr Gln Ile Met Val Glu
1 5 10 15
Ser Phe Val Asp Gly Asp Lys Gln Val Gly His Gly Thr Gly Tyr Gly
20 25 30
Thr Ser His His Lys Gly Asp Leu Gln Gly Ile Ile Asp Ser Leu Asp
35 40 45
Tyr Ile Gln Ser Leu Gly Val Asn Ala Ile Trp Leu Thr Pro Ile Phe
50 55 60
Glu Ser Ile Pro Val Glu Gly Gln Asp His Trp Ala Asp Arg Leu Asp
65 70 75 80
Ala Thr Gly Tyr Phe Ala Ser Asp Tyr Phe Lys Ile Asp Pro Arg Phe
85 90 95
Gly Thr Leu Glu Gln Ala Arg Glu Leu Val Glu Lys Ala His Ala Lys
100 105 110
Gly Leu Tyr Val Phe Phe Asp Gly Val Phe Gly His His Lys Gly Asn
115 120 125
Val Val Pro Ser Pro Gln Gly Arg Leu Pro Val Gly Glu Asn Asn Pro
130 135 140
Val Ser Tyr Pro Glu Ser Leu Ala Phe Tyr Glu Glu Val Ala Ser Tyr
145 150 155 160
Trp Val Lys Glu Leu Lys Ile Asp Gly Trp Arg Leu Asp Gln Ala Tyr
165 170 175
Gln Val Pro Thr Asp Ala Trp Lys Ala Ile Arg Gln Ser Val Asp Glu
180 185 190
Ala Ser Gln Ser Val Thr Tyr Val Asn Asn Lys Gly Glu Thr Val His
195 200 205
Pro Leu Gly Tyr Met Val Ala Glu Ile Trp Asn Asn Glu Arg Tyr Ile
210 215 220
Thr Glu Thr Gly Tyr Gly Lys Glu Gly Asp Pro Ala Leu Cys Ser Ala
225 230 235 240
Phe Asp Phe Pro Met Arg Phe Arg Val Val Glu Thr Phe Ala Val Asn
245 250 255
Glu Ser Gly Val Ser Arg Lys Gly Gly Glu Trp Leu Asn Asp Gly Met
260 265 270
Ser Leu His Ser Gln Tyr Pro Asp His Ala Lys Pro Asn Leu Met Leu
275 280 285
Gly Asn His Asp Val Val Arg Phe Gly Asp Leu Leu Gln Arg Gly Gly
290 295 300
Ile Ala Ser Pro Glu Gln Pro Gln Tyr Trp Gln Arg His Lys Ala Ala
305 310 315 320
Met Ser Phe Leu Ala Ala Tyr Thr Gly Pro Ile Thr Leu Tyr Tyr Gly
325 330 335
Glu Glu Ile Gly Asp Gln Val Asp Gly Phe Ala Lys Lys Ile Lys Glu
340 345 350
Asp Cys Ala Val Ile Gly Leu Cys Asp Asp His Val Ala Arg Thr Ser
355 360 365
Ala Lys Ile Asp Gly Val Thr Ala Ser Leu Asn Ala Gln Gln Ser Glu
370 375 380

```
Leu Lys Val Tyr Val Ser Ser Leu Met Thr Leu Arg Gln Gln His Pro
385                 390                 395                 400
Ala Leu Ser Gln Gly Glu Arg Thr Asn Val Met Ala Thr Glu Thr Val
                405                 410                 415
Tyr Val Asp His Lys Gln Ala Asp Asn Glu Ala Leu Leu Tyr Met Val
            420                 425                 430
Ser Thr Thr Asp Asn Ala Glu Ser Val Thr Leu Lys Gly Lys Ala Ile
        435                 440                 445
Gly Ser Gln Gly Val Leu Ile Asp Leu Leu Thr Asn Glu Arg Phe Met
    450                 455                 460
Pro Asn Asn Gly Glu Tyr Ala Ile Pro Leu Thr Gly Phe Gly Ala Arg
465                 470                 475                 480
Phe Leu Lys Ile Asp Thr Pro Thr Ala Ala Gly Val Met Ala Gln Ser
                485                 490                 495
Ala Ala Ser Val Ser Leu Val Gly Glu Gly Ile Met Ala Gln Cys Asp
            500                 505                 510
Thr Pro Thr Val Glu Gly Thr Gly Pro Val Ala Glu Thr Leu Tyr Val
        515                 520                 525
Val Gly Asp Phe Ala Asp Ala Gly Trp Lys Gln Lys Pro Gln Arg Ala
    530                 535                 540
Tyr Gln Tyr Lys Gly Lys His Asn Gly Ser Asn Leu Tyr Gln Val Val
545                 550                 555                 560
Val Asp Glu Lys Ala Gly Ala Tyr Lys Met Gln Tyr Ala Thr Lys Asp
                565                 570                 575
Trp Ser Pro Gln Phe Thr Ala Asp Gly Met Ala Leu Lys Pro Gly Thr
            580                 585                 590
Ala Lys Ser Leu Ile Ala Gly Gly Tyr Gly Lys Asp Thr Ala Val Thr
        595                 600                 605
Leu Pro Glu Ser Gly Lys Tyr Val Trp Ser Leu Thr Phe Ser Asp Leu
    610                 615                 620
Gly Glu Pro Glu Gln Ile
625                 630
```

<210> 203
<211> 2601
<212> DNA
<213> Environmental

<400> 203

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atgaagatga agtcccgggc gtggttgtta ggtagtgcag tggccatggc gttggcctct      60
tcggcagcca atgccggtgt catggttcac ctgttccagt ggaagtacaa tgacatcgcc     120
aacgagtgcg aaaaggtgct cggtcccaaa gggtatgaag cagtgcagat cacgccgcct     180
gctgaacacc tgcaaggctc ctcctggtgg gtggtctatc agcccgtcag ctacaagaac     240
ttcacttctc tgggcggtaa cgaggccgaa ctcaaaagca tgatcgcccg ttgcaaggcc     300
gccggggtca agatttacgc cgatgcggta ttcaaccagc tggctggtgg atcaggcgtc     360
ggtacaggtg gtagcagcta caatgccggc agcttcagct atccccaatt tggctacaac     420
gatttccatc acgctgggag cctcaccaac tatgccgacc gcaacaatgt gcaaaacggt     480
gccctgctgg ggctgccgga tctggatacc ggctctgcct atgtgcagga tcagctggct     540
acctatatga agaccctgag tggctggggt gtggcaggtt ttcgtcttga tgcagcaaag     600
catatgagcg ttgccgatct ctcggccatc gtcagcaagg cgggcaatcc ttttgtctac     660
tccgaggtga ttggtgccac gggtgaacca atccagccgg gcgaatatac cggcattggt     720
gccgtgaccg aatttaaata cggcaccgat ctggcctcca acttcaaggg gcagatcaag     780
aatctcaaga gcatgggcga gagctggggt ctgcttgcgt cgaacaaggc tgaagtcttt     840
gtggtcaacc atgaccgtga gcggggacat ggcggtggcg gtatgctgac ctacaaggat     900
ggtgccctct acaatctggc caacatcttc atgctggcct ggccctatgg cgcctatccc     960
caggtgatgt ccggctatga tttcggcacc aataccgata ttggtgggcc gagcgctacc    1020
ccttgttctt ccggctctag ctggaactgc gaacaccgct ggagcaacat cgccaacatg    1080
```

```
gtctcgttcc acaatgccgc ccaaggcacg tccatgacca actggtggga taatggtaat    1140
aaccagatcg cctttggtcg cggcgccaag gcctttgtgg tgatcaacaa tgaatcttcc    1200
actctgagca agagcctgca gacgggtctg ccagccgggg agtactgcaa cattctggcc    1260
ggtgatgccc tgtgcagcgg cagcaccatc aaggtggatg ccagcggtat ggccaccttc    1320
aacgtggcag ggatgaaggc ggcagcgatc catatcaatg ccaagcccga tagcaccagc    1380
agtggcagct caggctcttc ctctggctct tcttcctctg ccaccagtaa caagtttgcc    1440
agcatgaatc tgcggggcac caacaatggc tgggccagca ccgccatgac agtggatgcc    1500
aaccgtgtct ggtcggcgga tgtcaccttt accggggccg cggatgccaa tggtgcccag    1560
cgcttcaagt ttgatgtcta tggcaactgg acagagagct atggcgatac acaagccgat    1620
ggcattgccg acaaggggag cgccaaggac atctatttca atggtgtggg caagtatcgt    1680
gtctcgctca aggagagcga catgagctac accctgaccc agctctccag caatcaggca    1740
ccggtggcgg ccatcacccc caagacactc tccgtcaagc tgggtgactc agtggtgttc    1800
gatgcctccg gctccaccga tgatgtgggt gtcactggct acagctggtc taccggtggc    1860
agtgccaaga ccgaaactgt gctgtttgat gctctgggta ccaagaccat taccgtgaca    1920
gtggccgatg ccgatggctt gacctccaag gccagtgcca ccgtcaccgt caccgatggc    1980
agcgtggctt ataacagcaa ctttgccagc ctgaacttcc gtggcactcc caacagttgg    2040
ggcgcggcag ccatgacgct ggtggcagac aacacctggg aggcaacggt caacttcgat    2100
ggtcaggcca atcagcgctt caagttcgat atcaagggtg actggagcca gaactatggt    2160
gatagcaaca aggatggggt ggccgaacgt accggtgccg atatttacac cactgtgacc    2220
ggtcaatata aggtgcaatt taacgactcc actttgaagt acaccctgac caagctggcc    2280
gatagcagcg ccaccagcta tagcgcgaac tttgccagcc tctacctgcg tggcaccccg    2340
aacagctggg gcaccaccgc catgaagctg gtggccaata acagctggca ggccgaggtg    2400
accttcaccg gcaagggcga tgccactggt gcccaacgct tcaagttcga cgtcaagggt    2460
gactggagcc agaactacgg tgacagcaac atggacggga ctgccgaacg gactggtggc    2520
gatatcacca gtgccgtggt gggcacctat ctggtgacct ttaatgacag cacactgaaa    2580
tacaccctga ccgccaaata a                                              2601
```

<210> 204
<211> 866
<212> PRT
<213> Environmental

<400> 204

```
Met Lys Met Lys Ser Arg Ala Trp Leu Leu Gly Ser Ala Val Ala Met
 1               5                  10                  15
Ala Leu Ala Ser Ser Ala Ala Asn Ala Gly Val Met Val His Leu Phe
            20                  25                  30
Gln Trp Lys Tyr Asn Asp Ile Ala Asn Glu Cys Glu Lys Val Leu Gly
        35                  40                  45
Pro Lys Gly Tyr Glu Ala Val Gln Ile Thr Pro Pro Ala Glu His Leu
    50                  55                  60
Gln Gly Ser Ser Trp Trp Val Val Tyr Gln Pro Val Ser Tyr Lys Asn
65                  70                  75                  80
Phe Thr Ser Leu Gly Gly Asn Glu Ala Glu Leu Lys Ser Met Ile Ala
                85                  90                  95
Arg Cys Lys Ala Ala Gly Val Lys Ile Tyr Ala Asp Ala Val Phe Asn
            100                 105                 110
Gln Leu Ala Gly Gly Ser Gly Val Gly Thr Gly Gly Ser Ser Tyr Asn
        115                 120                 125
Ala Gly Ser Phe Ser Tyr Pro Gln Phe Gly Tyr Asn Asp Phe His His
    130                 135                 140
Ala Gly Ser Leu Thr Asn Tyr Ala Asp Arg Asn Asn Val Gln Asn Gly
145                 150                 155                 160
Ala Leu Leu Gly Leu Pro Asp Leu Asp Thr Gly Ser Ala Tyr Val Gln
                165                 170                 175
Asp Gln Leu Ala Thr Tyr Met Lys Thr Leu Ser Gly Trp Gly Val Ala
            180                 185                 190
```

```
Gly Phe Arg Leu Asp Ala Ala Lys His Met Ser Val Ala Asp Leu Ser
        195                 200                 205
Ala Ile Val Ser Lys Ala Gly Asn Pro Phe Val Tyr Ser Glu Val Ile
    210                 215                 220
Gly Ala Thr Gly Glu Pro Ile Gln Pro Gly Glu Tyr Thr Gly Ile Gly
225                 230                 235                 240
Ala Val Thr Glu Phe Lys Tyr Gly Thr Asp Leu Ala Ser Asn Phe Lys
                245                 250                 255
Gly Gln Ile Lys Asn Leu Lys Ser Met Gly Glu Ser Trp Gly Leu Leu
            260                 265                 270
Ala Ser Asn Lys Ala Glu Val Phe Val Val Asn His Asp Arg Glu Arg
        275                 280                 285
Gly His Gly Gly Gly Gly Met Leu Thr Tyr Lys Asp Gly Ala Leu Tyr
    290                 295                 300
Asn Leu Ala Asn Ile Phe Met Leu Ala Trp Pro Tyr Gly Ala Tyr Pro
305                 310                 315                 320
Gln Val Met Ser Gly Tyr Asp Phe Gly Thr Asn Thr Asp Ile Gly Gly
                325                 330                 335
Pro Ser Ala Thr Pro Cys Ser Ser Gly Ser Ser Trp Asn Cys Glu His
            340                 345                 350
Arg Trp Ser Asn Ile Ala Asn Met Val Ser Phe His Asn Ala Ala Gln
        355                 360                 365
Gly Thr Ser Met Thr Asn Trp Trp Asp Asn Gly Asn Asn Gln Ile Ala
    370                 375                 380
Phe Gly Arg Gly Ala Lys Ala Phe Val Val Ile Asn Asn Glu Ser Ser
385                 390                 395                 400
Thr Leu Ser Lys Ser Leu Gln Thr Gly Leu Pro Ala Gly Glu Tyr Cys
                405                 410                 415
Asn Ile Leu Ala Gly Asp Ala Leu Cys Ser Gly Ser Thr Ile Lys Val
            420                 425                 430
Asp Ala Ser Gly Met Ala Thr Phe Asn Val Ala Gly Met Lys Ala Ala
        435                 440                 445
Ala Ile His Ile Asn Ala Lys Pro Asp Ser Thr Ser Ser Gly Ser Ser
    450                 455                 460
Gly Ser Ser Ser Gly Ser Ser Ser Ser Ala Thr Ser Asn Lys Phe Ala
465                 470                 475                 480
Ser Met Asn Leu Arg Gly Thr Asn Asn Gly Trp Ala Ser Thr Ala Met
                485                 490                 495
Thr Val Asp Ala Asn Arg Val Trp Ser Ala Asp Val Thr Phe Thr Gly
            500                 505                 510
Ala Ala Asp Ala Asn Gly Ala Gln Arg Phe Lys Phe Asp Val Tyr Gly
        515                 520                 525
Asn Trp Thr Glu Ser Tyr Gly Asp Thr Gln Ala Asp Gly Ile Ala Asp
    530                 535                 540
Lys Gly Ser Ala Lys Asp Ile Tyr Phe Asn Gly Val Gly Lys Tyr Arg
545                 550                 555                 560
Val Ser Leu Lys Glu Ser Asp Met Ser Tyr Thr Leu Thr Gln Leu Ser
                565                 570                 575
Ser Asn Gln Ala Pro Val Ala Ala Ile Thr Pro Lys Thr Leu Ser Val
            580                 585                 590
Lys Leu Gly Asp Ser Val Val Phe Asp Ala Ser Gly Ser Thr Asp Asp
        595                 600                 605
Val Gly Val Thr Gly Tyr Ser Trp Ser Thr Gly Gly Ser Ala Lys Thr
    610                 615                 620
Glu Thr Val Leu Phe Asp Ala Leu Gly Thr Lys Thr Ile Thr Val Thr
625                 630                 635                 640
Val Ala Asp Ala Asp Gly Leu Thr Ser Lys Ala Ser Ala Thr Val Thr
```

```
                645                 650                 655
Val Thr Asp Gly Ser Val Ala Tyr Asn Ser Asn Phe Ala Ser Leu Asn
            660                 665                 670
Phe Arg Gly Thr Pro Asn Ser Trp Gly Ala Ala Ala Met Thr Leu Val
        675                 680                 685
Ala Asp Asn Thr Trp Glu Ala Thr Val Asn Phe Asp Gly Gln Ala Asn
    690                 695                 700
Gln Arg Phe Lys Phe Asp Ile Lys Gly Asp Trp Ser Gln Asn Tyr Gly
705                 710                 715                 720
Asp Ser Asn Lys Asp Gly Val Ala Glu Arg Thr Gly Ala Asp Ile Tyr
                725                 730                 735
Thr Thr Val Thr Gly Gln Tyr Lys Val Gln Phe Asn Asp Ser Thr Leu
            740                 745                 750
Lys Tyr Thr Leu Thr Lys Leu Ala Asp Ser Ser Ala Thr Ser Tyr Ser
        755                 760                 765
Ala Asn Phe Ala Ser Leu Tyr Leu Arg Gly Thr Pro Asn Ser Trp Gly
    770                 775                 780
Thr Thr Ala Met Lys Leu Val Ala Asn Asn Ser Trp Gln Ala Glu Val
785                 790                 795                 800
Thr Phe Thr Gly Lys Gly Asp Ala Thr Gly Ala Gln Arg Phe Lys Phe
                805                 810                 815
Asp Val Lys Gly Asp Trp Ser Gln Asn Tyr Gly Asp Ser Asn Met Asp
            820                 825                 830
Gly Thr Ala Glu Arg Thr Gly Gly Asp Ile Thr Ser Ala Val Val Gly
        835                 840                 845
Thr Tyr Leu Val Thr Phe Asn Asp Ser Thr Leu Lys Tyr Thr Leu Thr
    850                 855                 860
Ala Lys
865
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<210> 205
<211> 1674
<212> DNA
<213> Environmental

<400> 205

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atgtaccgcg taatacctat tattttgatt atgagtatga ttgtagcttg tgagtctcca      60
aagaaaaaaa caaccgaaac cgctcaacct tcaacaaatg ccgaaaaacc ctttgtttgg     120
gaggctgcca atgtatattt tttgttaact gaccgtttta acaacggtaa cccaaacaat     180
gacatcaatt ttaataggac taaagaatca ggaaaactcc gcaatttttat gggaggcgat     240
atcaagggca tcacccaaaa aataaatgag gggtatttta gtaaactagg cgttaatgcc     300
atctggctta ccccggttgt tgaacaaata catggcagtg ttgatgaagg taccggcaat     360
acctatgcct ttcatggcta ttgggccaaa gattggacaa acttagaccc aaatttttggc     420
acaaaagaag accttgccga actggtggca actgcccatg caaaaggcat caggatactt     480
ttagatgtgg taataaacca caccggcccg gtaaccgacc aagacccggt ttggggagaa     540
gattgggtac gtacaggccc gcagtgtacc tatgataatt acaccaatac caccagttgc     600
acgctggtag ccaatttacc tgatatactt acagaaagta atgaaaatgt ggccttacca     660
acctttttgt tagataaatg gaaagccgaa ggcagattag agcaagaact aaaagaactt     720
gacgattttt tttcccgcac aggccaccca cgcgcacccc gcttttacat tattaaatgg     780
cttaccgatt acatccgaga atttggggta gatgggttta gggttgatac cgtaaaacat     840
accgaagaaa cggtttgggc cgagttgtat gatgaagccg taattgcttt tgccgaatat     900
aaaaaagcca acccagacaa ggtattggac gataatgaat tttatatggt aggcgaagtg     960
tacaactacg gtatttccgg cggaaggttc tatgatttcg gcgataaaaa ggtggactat    1020
tttgaccacg gatttaaaag cctcatcaat tttgaaatga aatatgatgc caattttacc    1080
tacgatacac tttttaggaa gtacgatacc cttttgcata ccaaacttaa aggcagaagt    1140
gtgctcaact acctctcatc tcacgacgat ggaagtccat ttgataaaat gcggcaaaaa    1200
ccatacgagt cggctacaaa attactgctc actccgggcg catcccaaat ttattacggt    1260
```

```
gacgaaaccg ccagaagcct taacatagaa ggcgcacagg gagatgctac gcttcgttcg    1320
tttatgaatt gggaagagct cgcagaagac cctgccaagc aaaaaatact tcagcattgg    1380
caaaaactgg gcagtttcag gaacaaccac cccgcagttg gtgccggaag gcacaaaacc    1440
cttggcaaaa agccgtttta cacctttagc agggtttatc aaaaaaatgg ttttattgac    1500
aaagttgtgg tagcattaga tgcccctaaa ggccaaaaac aaattaccgt taatggtgtt    1560
tttgatgacg gtacaaaact tgtagatgcc tattcaggca aagaaacctc agttaaaaat    1620
ggtatcgttt cactttcttc tgaatttgat attgttttgt tagaacaaaa ataa          1674

<210> 206
<211> 557
<212> PRT
<213> Environmental

<400> 206
Met Tyr Arg Val Ile Pro Ile Ile Leu Ile Met Ser Met Ile Val Ala
 1               5                  10                  15
Cys Glu Ser Pro Lys Lys Lys Thr Thr Glu Thr Ala Gln Pro Ser Thr
            20                  25                  30
Asn Ala Glu Lys Pro Phe Val Trp Glu Ala Ala Asn Val Tyr Phe Leu
        35                  40                  45
Leu Thr Asp Arg Phe Asn Asn Gly Asn Pro Asn Asn Asp Ile Asn Phe
    50                  55                  60
Asn Arg Thr Lys Glu Ser Gly Lys Leu Arg Asn Phe Met Gly Gly Asp
65                  70                  75                  80
Ile Lys Gly Ile Thr Gln Lys Ile Asn Glu Gly Tyr Phe Ser Lys Leu
                85                  90                  95
Gly Val Asn Ala Ile Trp Leu Thr Pro Val Val Glu Gln Ile His Gly
            100                 105                 110
Ser Val Asp Glu Gly Thr Gly Asn Thr Tyr Ala Phe His Gly Tyr Trp
        115                 120                 125
Ala Lys Asp Trp Thr Asn Leu Asp Pro Asn Phe Gly Thr Lys Glu Asp
    130                 135                 140
Leu Ala Glu Leu Val Ala Thr Ala His Ala Lys Gly Ile Arg Ile Leu
145                 150                 155                 160
Leu Asp Val Val Ile Asn His Thr Gly Pro Val Thr Asp Gln Asp Pro
                165                 170                 175
Val Trp Gly Glu Asp Trp Val Arg Thr Gly Pro Gln Cys Thr Tyr Asp
            180                 185                 190
Asn Tyr Thr Asn Thr Thr Ser Cys Thr Leu Val Ala Asn Leu Pro Asp
        195                 200                 205
Ile Leu Thr Glu Ser Asn Glu Asn Val Ala Leu Pro Thr Phe Leu Leu
    210                 215                 220
Asp Lys Trp Lys Ala Glu Gly Arg Leu Glu Gln Glu Leu Lys Glu Leu
225                 230                 235                 240
Asp Asp Phe Phe Ser Arg Thr Gly His Pro Arg Ala Pro Arg Phe Tyr
                245                 250                 255
Ile Ile Lys Trp Leu Thr Asp Tyr Ile Arg Glu Phe Gly Val Asp Gly
            260                 265                 270
Phe Arg Val Asp Thr Val Lys His Thr Glu Glu Thr Val Trp Ala Glu
        275                 280                 285
Leu Tyr Asp Glu Ala Val Ile Ala Phe Ala Glu Tyr Lys Lys Ala Asn
    290                 295                 300
Pro Asp Lys Val Leu Asp Asp Asn Glu Phe Tyr Met Val Gly Glu Val
305                 310                 315                 320
Tyr Asn Tyr Gly Ile Ser Gly Gly Arg Phe Tyr Asp Phe Gly Asp Lys
                325                 330                 335
Lys Val Asp Tyr Phe Asp His Gly Phe Lys Ser Leu Ile Asn Phe Glu
```

```
            340                 345                 350
Met Lys Tyr Asp Ala Asn Phe Thr Tyr Asp Thr Leu Phe Arg Lys Tyr
        355                 360                 365
Asp Thr Leu Leu His Thr Lys Leu Lys Gly Arg Ser Val Leu Asn Tyr
    370                 375                 380
Leu Ser Ser His Asp Asp Gly Ser Pro Phe Asp Lys Met Arg Gln Lys
385                 390                 395                 400
Pro Tyr Glu Ser Ala Thr Lys Leu Leu Leu Thr Pro Gly Ala Ser Gln
                405                 410                 415
Ile Tyr Tyr Gly Asp Glu Thr Ala Arg Ser Leu Asn Ile Glu Gly Ala
            420                 425                 430
Gln Gly Asp Ala Thr Leu Arg Ser Phe Met Asn Trp Glu Glu Leu Ala
        435                 440                 445
Glu Asp Pro Ala Lys Gln Lys Ile Leu Gln His Trp Gln Lys Leu Gly
    450                 455                 460
Ser Phe Arg Asn Asn His Pro Ala Val Gly Ala Gly Arg His Lys Thr
465                 470                 475                 480
Leu Gly Lys Lys Pro Phe Tyr Thr Phe Ser Arg Val Tyr Gln Lys Asn
                485                 490                 495
Gly Phe Ile Asp Lys Val Val Val Ala Leu Asp Ala Pro Lys Gly Gln
            500                 505                 510
Lys Gln Ile Thr Val Asn Gly Val Phe Asp Asp Gly Thr Lys Leu Val
        515                 520                 525
Asp Ala Tyr Ser Gly Lys Glu Thr Ser Val Lys Asn Gly Ile Val Ser
    530                 535                 540
Leu Ser Ser Glu Phe Asp Ile Val Leu Leu Glu Gln Lys
545                 550                 555
```

<210> 207
<211> 1378
<212> DNA
<213> Environmental

<400> 207

```
ctgtcgactg agcctttcgt tttgggctcg agactgactc tcagcccacc ccgcagtagc      60
tccagacgga gtagccgtaa tagccgttgg ccgggtcgtg ggcaggggcc tcgaggtaca     120
cccacccgct tgagtccacc cacttgtcca cccagccgcc gaggttgccg gtgtactcgt     180
ggatgcacgc tcccgcgaac ttcggaacgt agacccacct tccggctttg cttgaggcga     240
ggttgatgta tgttatcagt cccggcttgc ttccgtagcc gtttctcacg aatatcagct     300
cgtcgttgtc gtagtaaacg acgtcagtgc ttcctccggc caggttgtca tgtatccaga     360
tgaggttctt gagcttatcc ttgttgagcc actcctcgta gtcgcggtag aatattgtcg     420
gctggccctc gtaggtgagg atgaacgcgt aggctggata cttgttccag attatatcgg     480
tgtcgtggtt tgcaacgaag gttacggcct taaacgggtc gcggctgacg actgtgcccc     540
cgttcttgag ggcctcgacg agtgcgggaa tgttcttgtt gtcaaaggcc gcgtccatct     600
tgtagtagag cgggaagtcg aagaccttgg cgccgctcga gtaggcccag ttgaggagtg     660
catcaacgtt ggtgtcccag tactcgccaa cggcccagcc gccccaccag ttgagccagt     720
ccttgacgac ccacgctccg tggcccttca cgtagtcaaa gcgccaggca tcaacgccga     780
tgctccttag gtaggcggcg tagctctcat cgctcgccca gagccagtgc tggtcccagc     840
tcttctcgtg ggctatgtct gggaagcctc caaatgtgcc ctcgtcacag cacttgacct     900
cgttggggtg gaagtcgagg tagttggcag tatatttgcc cgaggccacc tttgagaagt     960
ccgtccaggt gtagtcccca acgaacgggt tccactcgag gtctccgcct gcgcggtggt    1020
ttatgacgat gtccgctatg acctttatgc cgtaggcatg ggccgtgttt atcatgttca    1080
cgagctcctg cttggagcca aagcgcgtct ctaccgttcc cttctggtcg tactcaccga    1140
ggtcaaagaa gtcgtagggg tcgtagccca tcgaataggc gccgcccatg cccttgctcg    1200
ccgggggaat ccaaatggcg gatattcccg cctcgtacca ctccggtatc ttgctcctga    1260
tggtgtccca ccagattcct ccacctggga cgtcccagta gaaggcctgc attataacgc    1320
cgccctcttc cagctcggag tacttggcca taagttacct cctactagta gattaaaa      1378
```

<210> 208
<211> 439
<212> PRT
<213> Environmental

<400> 208
Leu Ser Thr Glu Pro Phe Val Leu Gly Ser Arg Leu Thr Leu Ser Pro
1 5 10 15
Pro Arg Ser Ser Ser Arg Arg Ser Ser Arg Asn Ser Arg Trp Pro Gly
20 25 30
Arg Gly Gln Gly Pro Arg Gly Thr Pro Thr Arg Leu Ser Pro Pro Thr
35 40 45
Cys Pro Pro Ser Arg Arg Gly Cys Arg Cys Thr Arg Gly Cys Thr Leu
50 55 60
Pro Arg Thr Ser Glu Arg Arg Pro Thr Phe Arg Leu Cys Leu Arg Arg
65 70 75 80
Gly Cys Met Leu Ser Val Pro Ala Cys Phe Arg Ser Arg Phe Ser Arg
85 90 95
Ile Ser Ala Arg Arg Cys Arg Ser Lys Arg Arg Gln Cys Phe Leu Arg
100 105 110
Pro Gly Cys His Val Ser Arg Gly Ser Ala Tyr Pro Cys Ala Thr Pro
115 120 125
Arg Ser Arg Gly Arg Ile Leu Ser Ala Gly Pro Arg Arg Gly Thr Arg
130 135 140
Arg Leu Asp Thr Cys Ser Arg Leu Tyr Arg Cys Arg Gly Leu Gln Arg
145 150 155 160
Arg Leu Arg Pro Thr Gly Arg Gly Arg Leu Cys Pro Arg Ser Gly Pro
165 170 175
Arg Arg Val Arg Glu Cys Ser Cys Cys Gln Arg Pro Arg Pro Ser Cys
180 185 190
Ser Arg Ala Gly Ser Arg Arg Pro Trp Arg Arg Ser Ser Arg Pro Ser
195 200 205
Gly Val His Gln Arg Trp Cys Pro Ser Thr Arg Gln Arg Pro Ser Arg
210 215 220
Pro Thr Ser Ala Ser Pro Arg Pro Thr Leu Arg Gly Pro Ser Arg Ser
225 230 235 240
Gln Ser Ala Arg His Gln Arg Arg Cys Ser Leu Gly Arg Arg Arg Ser
245 250 255
Ser His Arg Ser Pro Arg Ala Ser Ala Gly Pro Ser Ser Ser Arg Gly
260 265 270
Leu Cys Leu Gly Ser Leu Gln Met Cys Pro Arg His Ser Thr Pro Arg
275 280 285
Trp Gly Gly Ser Arg Gly Ser Trp Gln Tyr Ile Cys Pro Arg Pro Pro
290 295 300
Leu Arg Ser Pro Ser Arg Cys Ser Pro Gln Arg Thr Gly Ser Thr Arg
305 310 315 320
Gly Leu Arg Leu Arg Gly Gly Leu Arg Cys Pro Leu Pro Leu Cys Arg
325 330 335
Arg His Gly Pro Cys Leu Ser Cys Ser Arg Ala Pro Ala Trp Ser Gln
340 345 350
Ser Ala Ser Leu Pro Phe Pro Ser Gly Arg Thr His Arg Gly Gln Arg
355 360 365
Ser Arg Arg Gly Arg Ser Pro Ser Asn Arg Arg Arg Pro Cys Pro Cys
370 375 380
Ser Pro Gly Glu Ser Lys Trp Arg Ile Phe Pro Pro Arg Thr Thr Pro
385 390 395 400

```
Val Ser Cys Ser Trp Cys Pro Thr Arg Phe Leu His Leu Gly Arg Pro
                405                 410                 415
Ser Arg Arg Pro Ala Leu Arg Arg Pro Leu Pro Ala Arg Ser Thr Trp
            420                 425                 430
Pro Val Thr Ser Tyr Ile Lys
        435
```

<210> 209
<211> 1416
<212> DNA
<213> Environmental

<400> 209

```
atgattcagc ccatgcactc tcgggaacag gcctgccgtc tcattccggc actgatcatg      60
acatttgcac tggcactgcc gttgcaaatt cgtgccgatg tcaccctgca tgctttcaac     120
tggagctatg ccgatgtcgc tgatcgggcc gttgacatcg ctgcagcagg gtacagtgcc     180
gtgctggtgg ccccgccact tcgatccgaa ggcacggcct ggtgggcgcg ataccagccc     240
caggatctcc gccttatcga ccatccgctg ggcaatacac atgacttcgt caacatgatc     300
gatgctctcg atgatgtggg tgtgggcgtg tacgccgaca tcgtgctcaa ccacatggcc     360
aatgaggctg cacaaaggcc tgacctgaac taccctggtc aggcagtgct tgacgaatat     420
gcttccgatc ccggtcattt cgagggcttg aggctgttcg gtaatctgag cttcaatttc     480
ctgtcggaac atgatttcgg acccgcccag tgcattcagg attacagcga tgtgtttcag     540
gtccagaact ggcggctgtg cggaccgccg ccggacccgg gcctgcccga cctggtcgcc     600
aatgactggg tgatctctca acagcgccag tatctggaag ccatcaaggc gctgggtgtg     660
gctggcatgc gcatcgacgc ggtcaagcat atgcccatga gccatatcaa tgccgttctc     720
acccccgaga tccggtcggg cttgcatgtg tttggcgaag tcatcacctc cggtggggct     780
ggtgatacat cctacgaccg ttttctggcc ccttacctgg cacaaagcga ccatggtgcc     840
tatgactttc cattgtttga aaccattcgc cgtgctttcg gcttcggtgg cagcatgagt     900
gaactggtcg atcctgctgc ctacggtcag gccctgccac cggaccgcgc catcaccttc     960
gtcatcacgc acgatattcc gaacaatgac ggatttcgct accagatact cgaccccgtc    1020
gatgaatcac tggcctacgc ctacattctg ggccgcgatg gcggtgtccc gcttctgtat    1080
tccgacaaca atgaaagcgg cgatggccgc tggatcgatg cctggcaacg tccggatctg    1140
gttgcaatgg tcggcttcca caatgcagtc cacggtcagg acatggccgt gctttcacat    1200
gacgactgcc acctgctgtt tcggcgcggc agcctcggga ttgtcggcat caacaagtgc    1260
ggccatgcac tcagctcctg ggtcaacatg aaccagagcg tactgtggtg gtacgcggac    1320
tacacagacg tgctcgacag caacagcgtt gtcaacatcc agtcatcctg gcacgagttc    1380
atccttcccg cccgccaggc acgcctgtgg ttgcga                              1416
```

<210> 210
<211> 472
<212> PRT
<213> Environmental

<400> 210

```
Met Ile Gln Pro Met His Ser Arg Glu Gln Ala Cys Arg Leu Ile Pro
 1               5                  10                  15
Ala Leu Ile Met Thr Phe Ala Leu Ala Leu Pro Leu Gln Ile Arg Ala
            20                  25                  30
Asp Val Thr Leu His Ala Phe Asn Trp Ser Tyr Ala Asp Val Ala Asp
        35                  40                  45
Arg Ala Val Asp Ile Ala Ala Ala Gly Tyr Ser Ala Val Leu Val Ala
    50                  55                  60
Pro Pro Leu Arg Ser Glu Gly Thr Ala Trp Trp Ala Arg Tyr Gln Pro
65                  70                  75                  80
Gln Asp Leu Arg Leu Ile Asp His Pro Leu Gly Asn Thr His Asp Phe
                85                  90                  95
Val Asn Met Ile Asp Ala Leu Asp Asp Val Gly Val Gly Val Tyr Ala
```

```
            100                 105                 110
Asp Ile Val Leu Asn His Met Ala Asn Glu Ala Ala Gln Arg Pro Asp
        115                 120                 125
Leu Asn Tyr Pro Gly Gln Ala Val Leu Asp Glu Tyr Ala Ser Asp Pro
    130                 135                 140
Gly His Phe Glu Gly Leu Arg Leu Phe Gly Asn Leu Ser Phe Asn Phe
145                 150                 155                 160
Leu Ser Glu His Asp Phe Gly Pro Ala Gln Cys Ile Gln Asp Tyr Ser
                165                 170                 175
Asp Val Phe Gln Val Gln Asn Trp Arg Leu Cys Gly Pro Pro Pro Asp
            180                 185                 190
Pro Gly Leu Pro Asp Leu Val Ala Asn Asp Trp Val Ile Ser Gln Gln
        195                 200                 205
Arg Gln Tyr Leu Glu Ala Ile Lys Ala Leu Gly Val Ala Gly Met Arg
    210                 215                 220
Ile Asp Ala Val Lys His Met Pro Met Ser His Ile Asn Ala Val Leu
225                 230                 235                 240
Thr Pro Glu Ile Arg Ser Gly Leu His Val Phe Gly Glu Val Ile Thr
                245                 250                 255
Ser Gly Gly Ala Gly Asp Thr Ser Tyr Asp Arg Phe Leu Ala Pro Tyr
            260                 265                 270
Leu Ala Gln Ser Asp His Gly Ala Tyr Asp Phe Pro Leu Phe Glu Thr
        275                 280                 285
Ile Arg Arg Ala Phe Gly Phe Gly Gly Ser Met Ser Glu Leu Val Asp
    290                 295                 300
Pro Ala Ala Tyr Gly Gln Ala Leu Pro Pro Asp Arg Ala Ile Thr Phe
305                 310                 315                 320
Val Ile Thr His Asp Ile Pro Asn Asn Asp Gly Phe Arg Tyr Gln Ile
                325                 330                 335
Leu Asp Pro Val Asp Glu Ser Leu Ala Tyr Ala Tyr Ile Leu Gly Arg
            340                 345                 350
Asp Gly Gly Val Pro Leu Leu Tyr Ser Asp Asn Asn Glu Ser Gly Asp
        355                 360                 365
Gly Arg Trp Ile Asp Ala Trp Gln Arg Pro Asp Leu Val Ala Met Val
    370                 375                 380
Gly Phe His Asn Ala Val His Gly Gln Asp Met Ala Val Leu Ser His
385                 390                 395                 400
Asp Asp Cys His Leu Leu Phe Arg Arg Gly Ser Leu Gly Ile Val Gly
                405                 410                 415
Ile Asn Lys Cys Gly His Ala Leu Ser Ser Trp Val Asn Met Asn Gln
            420                 425                 430
Ser Val Leu Trp Trp Tyr Ala Asp Tyr Thr Asp Val Leu Asp Ser Asn
        435                 440                 445
Ser Val Val Asn Ile Gln Ser Ser Trp His Glu Phe Ile Leu Pro Ala
    450                 455                 460
Arg Gln Ala Arg Leu Trp Leu Arg
465                 470
```

<210> 211
<211> 1491
<212> DNA
<213> Environmental

<400> 211
gtgtttcgtt ctgacacagt ttcgcgtacc tgcatgtatg gtgcgctgcg taatgcctac 60
caacccgatc gggtgtttac tggagtcacg gtgcggacat gcaacttaaa aaagcatgct 120
catcgccagg cgctgttgtt catcgtgacg cggtgcctgt gcctgaaatc caggcagacc 180

```
cataaaaaca acaacaaacc gataacaaac gacccaagcc ttctaagagg agaaaacggg     240
atggctttta aactacgcaa aaaggcgctc gttggcctgt tcacggccgg cgcaatggta     300
tatgccggtg cagcggcgag tggtgaaatc attctgcagg gcttccactg gcactccaag     360
tggggcggca acaatcaggg ttggtggcag gtgatggaag gtcaggccaa caccatcgcc     420
aacgccggct ttacgcacgt gtggttcccg ccggtccata actcggccga tgccgagggt     480
tacctacccc gcgagctgaa caacctcaac tccagctatg gctccgaagc acagctgcgc     540
agcgccatcc aggcactgaa caatcgcggc gtgcatgcga ttgccgatgt ggtcatgaac     600
caccgggtgg gctgctctgg ctgggcggat ttctgtaacc cggactggcc gacctggtac     660
atcgtcgcca atgattcctg gcccggtggc ccgaaaagcc agaactggga cacgggtgag     720
acgtaccacg ccgcccgtga cctcgatcac gccaatccgc aggtgcgcaa cgatatctcg     780
cactacctga acagccgcct caaggacgtc ggcttctccg gctggcgctg ggactatgcc     840
aagggtttct ggcccggcta tgtcggcgag tacaactgga acaccaaccc gaacttctgt     900
gtgggtgagg tgtgggacga tctcgacccc aacaatccca acccgcaccg ccagcaactg     960
gtggactggg ttgatgctac cggtggcagt tgtcacgtct tcgacttcac caccaagggg    1020
ctgacgaact atgcgctgca gcatggccag tactggcgcc tgcagggtga taatggtggc    1080
ccggctggcg gcatcggctg gtggccgcaa cgcatggtga ccttcgtcga caaccatgac    1140
acgggcccga gcaatcactg tggtgacggc cagaacctct ggcccgtgcc ctgtgacaag    1200
gtcatggagg cgtatgccta catcctgacc catccgggcg tgccgtcggt gtactggacg    1260
cacttcttca actggaatct tggtagcgag atcagccagt tgatgcagat ccgcaagaac    1320
cagggcgtgc actccggttc cgacgtctgg atcgccgagg cccgtcacgg cctgtacgcc    1380
gcctatatca acggtaatgt ggcgatgaag atgggctggg ataactggag cccgggctgg    1440
ggctggtcgc tggcggcctc cggtaacaac tgggccgtct ggacacgctg a              1491
```

<210> 212
<211> 496
<212> PRT
<213> Environmental

<400> 212

```
Val Phe Arg Ser Asp Thr Val Ser Arg Thr Cys Met Tyr Gly Ala Leu
 1               5                  10                  15
Arg Asn Ala Tyr Gln Pro Asp Arg Val Phe Thr Gly Val Thr Val Arg
            20                  25                  30
Thr Cys Asn Leu Lys Lys His Ala His Arg Gln Ala Leu Leu Phe Ile
        35                  40                  45
Val Thr Arg Cys Leu Cys Leu Lys Ser Arg Gln Thr His Lys Asn Asn
    50                  55                  60
Asn Lys Pro Ile Thr Asn Asp Pro Ser Leu Leu Arg Gly Glu Asn Gly
65                  70                  75                  80
Met Ala Phe Lys Leu Arg Lys Lys Ala Leu Val Gly Leu Phe Thr Ala
                85                  90                  95
Gly Ala Met Val Tyr Ala Gly Ala Ala Ala Ser Gly Glu Ile Ile Leu
            100                 105                 110
Gln Gly Phe His Trp His Ser Lys Trp Gly Gly Asn Asn Gln Gly Trp
        115                 120                 125
Trp Gln Val Met Glu Gly Gln Ala Asn Thr Ile Ala Asn Ala Gly Phe
    130                 135                 140
Thr His Val Trp Phe Pro Pro Val His Asn Ser Ala Asp Ala Glu Gly
145                 150                 155                 160
Tyr Leu Pro Arg Glu Leu Asn Asn Leu Asn Ser Ser Tyr Gly Ser Glu
                165                 170                 175
Ala Gln Leu Arg Ser Ala Ile Gln Ala Leu Asn Asn Arg Gly Val His
            180                 185                 190
Ala Ile Ala Asp Val Val Met Asn His Arg Val Gly Cys Ser Gly Trp
        195                 200                 205
Ala Asp Phe Cys Asn Pro Asp Trp Pro Thr Trp Tyr Ile Val Ala Asn
    210                 215                 220
```

```
Asp Ser Trp Pro Gly Gly Pro Lys Ser Gln Asn Trp Asp Thr Gly Glu
225                 230                 235                 240
Thr Tyr His Ala Ala Arg Asp Leu Asp His Ala Asn Pro Gln Val Arg
                245                 250                 255
Asn Asp Ile Ser His Tyr Leu Asn Ser Arg Leu Lys Asp Val Gly Phe
            260                 265                 270
Ser Gly Trp Arg Trp Asp Tyr Ala Lys Gly Phe Trp Pro Gly Tyr Val
        275                 280                 285
Gly Glu Tyr Asn Trp Asn Thr Asn Pro Asn Phe Cys Val Gly Glu Val
    290                 295                 300
Trp Asp Asp Leu Asp Pro Asn Asn Pro Asn Pro His Arg Gln Gln Leu
305                 310                 315                 320
Val Asp Trp Val Asp Ala Thr Gly Gly Ser Cys His Val Phe Asp Phe
                325                 330                 335
Thr Thr Lys Gly Leu Thr Asn Tyr Ala Leu Gln His Gly Gln Tyr Trp
            340                 345                 350
Arg Leu Gln Gly Asp Asn Gly Gly Pro Ala Gly Gly Ile Gly Trp Trp
        355                 360                 365
Pro Gln Arg Met Val Thr Phe Val Asp Asn His Asp Thr Gly Pro Ser
    370                 375                 380
Asn His Cys Gly Asp Gly Gln Asn Leu Trp Pro Val Pro Cys Asp Lys
385                 390                 395                 400
Val Met Glu Ala Tyr Ala Tyr Ile Leu Thr His Pro Gly Val Pro Ser
                405                 410                 415
Val Tyr Trp Thr His Phe Phe Asn Trp Asn Leu Gly Ser Glu Ile Ser
            420                 425                 430
Gln Leu Met Gln Ile Arg Lys Asn Gln Gly Val His Ser Gly Ser Asp
        435                 440                 445
Val Trp Ile Ala Glu Ala Arg His Gly Leu Tyr Ala Ala Tyr Ile Asn
    450                 455                 460
Gly Asn Val Ala Met Lys Met Gly Trp Asp Asn Trp Ser Pro Gly Trp
465                 470                 475                 480
Gly Trp Ser Leu Ala Ala Ser Gly Asn Asn Trp Ala Val Trp Thr Arg
                485                 490                 495
```

<210> 213
<211> 23
<212> PRT
<213> Environmental

<400> 213

```
Met Phe Leu Leu Ala Phe Leu Leu Thr Ala Ser Leu Phe Cys Pro Thr
 1               5                  10                  15
Gly Gln Pro Ala Lys Ala Ala
            20
```

<210> 214
<211> 23
<212> PRT
<213> Bacterial

<400> 214

```
Val Leu Thr Phe His Arg Ile Ile Arg Lys Gly Trp Met Phe Leu Leu
 1               5                  10                  15
Ala Phe Leu Leu Thr Ala Ser
            20
```

<210> 215
<211> 33
<212> PRT
<213> Bacterial

<400> 215
Met Lys Ser Phe Ala Phe Met Pro Ile Leu Phe Tyr Ala Asn Asp Phe
1 5 10 15
Ile Ser Glu Arg Glu Gly Gly Gly Lys Met Gly Lys Asn Met Arg Arg
20 25 30
Arg

<210> 216
<211> 31
<212> PRT
<213> Bacterical

<400> 216
Met Arg Lys Lys Met Ser His Ser Arg Phe Thr Phe Leu Leu Ile Leu
1 5 10 15
Ala Leu Phe Ile Phe Phe Ser Gly Cys Ile Ser Glu Val Lys Ser
20 25 30

<210> 217
<211> 30
<212> PRT
<213> Bacterial

<400> 217
Met Tyr Thr Leu Phe Ile Arg Ser Phe Tyr Asp Thr Asn Asn Asp Gly
1 5 10 15
Val Gly Asp Tyr Asn Gly Val Ala Gln Lys Val Asp Tyr Leu
20 25 30

<210> 218
<211> 22
<212> PRT
<213> Environmental

<400> 218
Val Leu Thr Phe His Arg Ile Ile Arg Lys Gly Trp Met Phe Leu Leu
1 5 10 15
Ala Phe Leu Leu Thr Ala
20

<210> 219
<211> 33
<212> PRT
<213> Environmental

<400> 219
Met Ser Leu Phe Lys Lys Ile Phe Pro Trp Ile Val Ser Leu Leu Leu
1 5 10 15
Leu Phe Ser Phe Ile Ala Pro Phe Ser Ile Gln Thr Glu Lys Val Arg
20 25 30
Ala

<210> 220
<211> 25
<212> PRT
<213> Environmental

<400> 220
Met Ala Arg Lys Thr Leu Ala Ile Phe Phe Val Leu Leu Val Leu Leu
1 5 10 15
Ser Leu Ser Ala Val Pro Ala Lys Ala
20 25

<210> 221
<211> 35
<212> PRT
<213> Environmental

<400> 221
Met Pro Ala Phe Lys Ser Lys Val Met His Met Lys Leu Lys Tyr Leu
1 5 10 15
Ala Leu Val Leu Leu Ala Val Ala Ser Ile Gly Leu Leu Ser Thr Pro
20 25 30
Val Gly Ala
35

<210> 222
<211> 28
<212> PRT
<213> Environmental

<400> 222
Met Lys Gln Gln Lys Arg Leu Tyr Ala Arg Leu Leu Thr Leu Leu Phe
1 5 10 15
Ala Leu Ile Phe Leu Leu Pro His Ser Ala Ala Ala
20 25

<210> 223
<211> 21
<212> PRT
<213> Environmental

<400> 223
Met Arg Val Phe Leu Val Val Pro Lys Leu Ser Arg Pro Phe Gln Ala
1 5 10 15
Glu Ser Gln Gln Gln
20

<210> 224
<211> 30
<212> PRT
<213> Bacterial

<400> 224
Met Gln Thr Phe Ala Phe Leu Phe Tyr Ser Lys Lys Gly Trp Val Cys
1 5 10 15
Met Asn Tyr Leu Lys Lys Val Trp Leu Tyr Tyr Ala Ile Val

```
            20                  25                  30

<210> 225
<211> 35
<212> PRT
<213> Environmental

<400> 225
Met Pro Gln Ala Ile Arg Thr Phe Ser Arg Trp Thr Leu Phe Gly Leu
 1               5                  10                  15
Ile Gly Val Phe Leu Leu Gly Leu Val Phe Ser Val Pro Pro Arg Ala
            20                  25                  30
Ile Gln Ala
        35

<210> 226
<211> 28
<212> PRT
<213> Environmental

<400> 226
Val Val His Met Lys Leu Lys Tyr Leu Ala Leu Val Leu Leu Ala Val
 1               5                  10                  15
Ala Ser Ile Gly Leu Leu Ser Thr Pro Val Gly Ala
            20                  25

<210> 227
<211> 30
<212> PRT
<213> Environmental

<400> 227
Val Cys Met Asn Tyr Leu Lys Lys Val Trp Leu Tyr Tyr Ala Ile Val
 1               5                  10                  15
Ala Thr Leu Ile Ile Tyr Phe Leu Thr Pro Phe Ser Thr Ala
            20                  25                  30

<210> 228
<211> 30
<212> PRT
<213> Environmental

<400> 228
Met Pro Gln Leu Tyr Pro Leu Pro Pro Arg Trp Arg Arg Ala Ala Arg
 1               5                  10                  15
Gln Gly Leu Ala Ala Leu Thr Leu Ala Thr Thr Ala Leu Gly
            20                  25                  30

<210> 229
<211> 30
<212> PRT
<213> Environmental

<400> 229
Met Asn Asn Val Lys Lys Val Trp Leu Tyr Tyr Ser Ile Ile Ala Thr
 1               5                  10                  15
Leu Val Ile Ser Phe Phe Thr Pro Phe Ser Thr Ala Gln Ala
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20 25 30

<210> 230
<211> 28
<212> PRT
<213> Environmental

<400> 230
Val Gly Arg Ala Gly Leu Ala His His Ser Asn Thr Ser Ala Lys Gly
1 5 10 15
Thr Tyr Gly Ser Pro Leu Glu Leu Arg Pro Asp Arg
20 25

<210> 231
<211> 23
<212> PRT
<213> Environmental

<400> 231
Met Lys Thr Phe Asn Leu Lys Pro Thr Leu Leu Pro Leu Thr Leu Leu
1 5 10 15
Leu Ser Ser Pro Val Leu Ala
20

<210> 232
<211> 23
<212> PRT
<213> Environmental

<400> 232
Met Lys Pro Ile Asn Thr Leu Leu Ile Ser Ala Leu Ala Val Cys Ser
1 5 10 15
Phe Ser Ser Ala Thr Tyr Ala
20

<210> 233
<211> 30
<212> PRT
<213> Environmental

<400> 233
Met Pro Lys Ser Thr Phe Thr Lys Ser Ile Thr Lys Ser Leu Leu Ala
1 5 10 15
Thr Ser Val Val Val Ser Leu Leu Pro Ala Tyr Ala Gln Ala
20 25 30

<210> 234
<211> 27
<212> PRT
<213> Environmental

<400> 234
Met Leu Lys Arg Ile Thr Val Val Cys Leu Leu Phe Ile Leu Leu Phe
1 5 10 15
Pro Asn Ile Tyr Gly Arg Asn Lys Ala Glu Ala
20 25

<210> 235
<211> 29
<212> PRT
<213> Environmental

<400> 235
Met Ser Leu Asn Asn Phe Lys Val Lys Leu Leu Ser Phe Ala Val Ser
1 5 10 15
Ser Ala Val Leu Ser Leu Ala Pro Asn Leu Ala Asn Ala
20 25

<210> 236
<211> 28
<212> PRT
<213> Environmental

<400> 236
Met Ile Leu Ser Asn Phe Lys Val Lys Leu Leu Ser Phe Ala Val Ser
1 5 10 15
Ser Ala Val Leu Thr Leu Ala Ala Asn Val Ala Asn
20 25

<210> 237
<211> 27
<212> PRT
<213> Environmental

<400> 237
Met Leu Lys Arg Ile Thr Val Val Cys Leu Leu Phe Ile Leu Leu Phe
1 5 10 15
Pro Asn Ile Tyr Glu Gly Asn Lys Ala Glu Ala
20 25

<210> 238
<211> 26
<212> PRT
<213> Environmental

<400> 238
Met Pro Ser Ile Asn Ala Ser Asp Cys Lys Lys Lys Gly Asp Arg Ser
1 5 10 15
Met Lys Arg Lys Lys Trp Thr Ala Leu Ala
20 25

<210> 239
<211> 33
<212> PRT
<213> Environmental

<400> 239
Val Ser Arg Met Phe Ala Lys Arg Phe Lys Thr Ser Leu Leu Pro Leu
1 5 10 15
Phe Ala Gly Phe Leu Leu Leu Phe His Leu Val Leu Ala Gly Pro Thr
20 25 30
Ala

<210> 240
<211> 25
<212> PRT
<213> Environmental

<400> 240
Met Gln Thr Ile Ala Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys
 1   5   10   15
Trp Thr Ala Leu Ala Leu Thr Leu Pro
            20   25

<210> 241
<211> 25
<212> PRT
<213> Environmental

<400> 241
Met Gln Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys Trp Thr Ala
 1   5   10   15
Leu Ala Leu Thr Leu Pro Leu Ala Ala
            20   25

<210> 242
<211> 36
<212> PRT
<213> Bacterical

<400> 242
Val Asp Pro Lys Asn Cys Ser Gln Phe Met Gln Thr Ile Ala Lys Lys
 1   5   10   15
Gly Asp Glu Thr Met Lys Gly Lys Lys Trp Thr Ala Leu Ala Leu Thr
            20   25   30
Leu Pro Leu Ala
        35

<210> 243
<211> 36
<212> PRT
<213> Environmental

<400> 243
Met Gln Thr Ile Ala Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys
 1   5   10   15
Trp Thr Ala Leu Ala Leu Thr Leu Pro Leu Ala Ala Ser Leu Ser Thr
            20   25   30
Gly Val His Ala
        35

<210> 244
<211> 23
<212> PRT
<213> Environmental

<400> 244
Met Lys Thr Phe Lys Leu Lys Arg Thr Phe Leu Pro Leu Thr Leu Leu
 1   5   10   15
Leu Ser Ala Pro Ala Phe Ala

20

<210> 245
<211> 25
<212> PRT
<213> Environmental

<400> 245
Met Gln Thr Ile Ala Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys
1 5 10 15
Trp Thr Ala Leu Ala Leu Thr Leu Pro
20 25

<210> 246
<211> 22
<212> PRT
<213> Environmental

<400> 246
Met Lys Asn Ile Ile Arg Leu Cys Ala Ala Ser Ala Ile Leu Thr Val
1 5 10 15
Ser His Ala Ser Tyr Ala
20

<210> 247
<211> 23
<212> PRT
<213> Environmental

<400> 247
Met Lys Thr Phe Lys Leu Lys Arg Thr Phe Leu Pro Leu Thr Leu Leu
1 5 10 15
Leu Ser Ala Pro Ala Phe Ala
20

<210> 248
<211> 23
<212> PRT
<213> Environmental

<400> 248
Met Lys Thr Phe Lys Leu Lys Arg Thr Phe Leu Pro Leu Thr Leu Leu
1 5 10 15
Leu Ser Ala Pro Ala Phe Ala
20

<210> 249
<211> 25
<212> PRT
<213> Environmental

<400> 249
Met Lys Leu Met Lys Gly Lys Lys Trp Thr Ala Leu Ala Leu Thr Leu
1 5 10 15
Pro Leu Ala Ala Ser Leu Ser Thr Gly
20 25

<210> 250
<211> 36
<212> PRT
<213> Environmental

<400> 250
Met Gln Thr Ile Ala Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys
 1   5   10   15
Trp Thr Ala Leu Ala Leu Thr Leu Pro Leu Ala Ala Ser Leu Ser Thr
            20   25   30
Gly Val His Ala
        35

<210> 251
<211> 25
<212> PRT
<213> Environmental

<400> 251
Met Gln Thr Ile Ala Lys Lys Gly Asp Glu Thr Met Lys Gly Lys Lys
 1   5   10   15
Trp Thr Ala Leu Ala Leu Thr Leu Pro
            20   25

<210> 252
<211> 25
<212> PRT
<213> Environmental

<400> 252
Met Lys Phe Lys Lys Ser Leu Ser Ala Gly Leu Leu Leu Phe Gly Gly
 1   5   10   15
Leu Ser Gly Val Thr Pro Ser Val Ala
            20   25

<210> 253
<211> 23
<212> PRT
<213> Environmental

<400> 253
Met Lys Pro Ser Lys Phe Val Phe Leu Ser Ala Ala Ile Ala Cys Ser
 1   5   10   15
Leu Ser Ser Thr Ala Asn Ala
            20

<210> 254
<211> 23
<212> PRT
<213> Environmental

<400> 254
Val Ser Leu Thr Lys Lys Ala Gln Tyr Glu Pro Asn Thr Ala Pro Arg
 1   5   10   15
Leu Ser Thr Ser Leu Gln Ser
            20

<210> 255
<211> 30
<212> PRT
<213> Environmental

<400> 255
Met Thr Ala Lys Ala Asp Asp Leu Arg Ile Tyr Gln Ile Met Val Glu
 1   5   10   15
Ser Phe Val Asp Gly Asp Lys Gln Val Gly His Gly Thr Gly
            20   25   30

<210> 256
<211> 25
<212> PRT
<213> Environmental

<400> 256
Met Lys Met Lys Ser Arg Ala Trp Leu Leu Gly Ser Ala Val Ala Met
 1   5   10   15
Ala Leu Ala Ser Ser Ala Ala Asn Ala
            20   25

<210> 257
<211> 16
<212> PRT
<213> Environmental

<400> 257
Met Tyr Arg Val Ile Pro Ile Ile Leu Ile Met Ser Met Ile Val Ala
 1   5   10   15

<210> 258
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 258
gaacactagt aggaggtaac ttatggcaaa gtattccgag ctcgaag 47

<210> 259
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 259
gaacggtctc attccgccag ccagcaaggg gatgagcgg 39

<210> 260
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 260
gaaccgtctc aaaacacggc ccatgcctac ggc 33

<210> 261
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 261
gaacgtctca cctcgacttc caccccaacg aggtcaag 38

<210> 262
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 262
gaacgtctca ggcgctttga ctacgtgaag ggc 33

<210> 263
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 263
gaacggtctc aacaagatgg atgaggcctt tg 32

<210> 264
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 264
gaaccgtctc acgatataat ctggaacaag taccttgc 38

<210> 265
<211> 35
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 265
gaaccgtctc agaagcacga gcatagttta ctacg 35

<210> 266
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 266
gaaccgtctc aaaggtgggt ttatgtgccg 30

<210> 267
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 267
gaacgtctca ggaatccaaa tggcggatat tcccgc 36

<210> 268
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 268
gaacggtctc agtttatcat attgatgagc tcc 33

<210> 269
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 269
gaaccgtctc agaggtagtt ggcagtatat ttg 33

<210> 270
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 270
gaacgtctca cgccaggcat caacgccgat g 31

<210> 271
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 271
gaacgtctca ttgtagtaga gcgggaagtc 30

<210> 272
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 272
gaacggtctc aatcggtgtc gtggtttgct ac 32

<210> 273
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 273
gaaccgtctc acttccacct gcgaggtggt c 31

<210> 274
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 274
gaaccgtctc accttccaac cttgctcgag c 31

<210> 275
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 275
tcgagactga ctctcaccca acaccgcaat agc 33

<210> 276
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 276
gaacactagt aggaggtaac ttatggccaa gtacctggag ctcgaagagg 50

<210> 277
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 277
gaacggtctc attcccccgg cgagcaaggg c 31

<210> 278
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 278
gaaccgtctc aaaacaccgc ccacgcctac gg 32

<210> 279
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 279
gaacgtctca cctcgacttc caccccaac 29

<210> 280
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 280
gaacgtctca ggcgcttcga ctacgtcaag g 31

<210> 281

<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 281
gaacggtctc aacaagatgg acgcggcctt tgac 34

<210> 282
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 282
gaaccgtctc acgatataat ttggaacaag taccc 35

<210> 283
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 283
gaaccgtctc agaagcaccg acatagtcta c 31

<210> 284
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 284
gaaccgtctc aaaggtgggt ctacgttccg 30

<210> 285
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 285
gaacgtctca ggaatccata ttgcggagat tccggc 36

<210> 286
<211> 32
<212> DNA

<213> Artificial Sequence

<220>
<223> primer

<400> 286
gaacggtctc agtttatcat gttcacgagc tc 32

<210> 287
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 287
gaaccgtctc agaggtagtt ggccgtgtac ttg 33

<210> 288
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 288
gaacgtctca gccatgcgtc aacgccgatg 30

<210> 289
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 289
gaacgtctca ttgtagtaga gcgggaagtc g 31

<210> 290
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 290
gaacggtctc aatcggtgtc gtggtttgca acg 33

<210> 291
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 291
gaaccgtctc acttccaccg gcgaggtggt cgtg 34

<210> 292
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 292
gaaccgtctc accttccggc cttgctcgag cc 32

<210> 293
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 293
tcgagactga ctctcagccc accccgcagt agctc 35

<210> 294
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 294
gaacactagt aggaggtaac ttatggccaa gtactccgag ctggaagagg 50

<210> 295
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 295
gaacggtctc attcctcccg cgagcaaggg 30

<210> 296
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 296
gaaccgtctc aaaacaccgc ccacgcctat g 31

<210> 297
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 297
gaacgtctca cctcgacttc cacccgaacg agc 33

<210> 298
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 298
gaacgtctca ggcgcttcga ctacgtcaag g 31

<210> 299
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 299
gaacggtctc aacaagatgg acgaggcctt cg 32

<210> 300
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 300
gaaccgtctc acgatataat ctggaacaag 30

<210> 301
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 301

gaaccgtctc agaagcactg acatcgttta ctacg 35

<210> 302
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 302
gaaccgtctc aaaggtgggt ttacgttccg 30

<210> 303
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 303
gaacgtctca ggaatccata tcgccgaaat 30

<210> 304
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 304
gaacggtctc agtttatcat gtttatgagc 30

<210> 305
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 305
gaaccgtctc agaggtagtt ggccgtgtat ttac 34

<210> 306
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 306
gaacgtctca cgccaggcat cgatgccgat 30

<210> 307
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 307
gaacgtctca ttgtagtaga gggcgaagtc aaag 34

<210> 308
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 308
gaacggtctc aatcggtatc gtggttggct acaaac 36

<210> 309
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 309
gaaccgtctc acttcctccg gcgaggttgt catg 34

<210> 310
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 310
gaaccgtctc accttccggc tttgcttgag gc 32

<210> 311
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 311
tcgagactga ctctcaccca acaccgcagt agctcc 36

<210> 312
<211> 38

<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 312
cacacagcag caaccaacct cgagactgac tctcascc 38

<210> 313
<211> 461
<212> PRT
<213> Pyrococcus sp.

<400> 313
Met Lys Lys Phe Val Ala Leu Leu Ile Thr Met Phe Phe Val Val Ser
 1   5   10   15
Met Ala Ala Val Ala Gln Pro Ala Ser Ala Ala Lys Tyr Ser Glu Leu
            20   25   30
Glu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Ala
        35   40   45
Gly Gly Ile Trp Trp Asp Thr Ile Arg Ser Lys Ile Pro Glu Trp Tyr
    50   55   60
Glu Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met
65   70   75   80
Gly Gly Ala Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu
                85   90   95
Gly Glu Tyr Asn Gln Lys Gly Thr Val Glu Thr Arg Phe Gly Ser Lys
            100   105   110
Gln Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys
        115   120   125
Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp Leu Glu
    130   135   140
Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val
145   150   155   160
Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu
                165   170   175
Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala
            180   185   190
His Glu Lys Glu Trp Asp Gln His Trp Leu Trp Ala Ser Asp Glu Ser
        195   200   205
Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp
    210   215   220
Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asn Trp
225   230   235   240
Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala
                245   250   255
Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe Asp Phe Pro
            260   265   270
Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Thr Asn Ile Pro Ala
        275   280   285
Leu Val Asp Ala Leu Gln Asn Gly Gly Thr Val Val Ser Arg Asp Pro
    290   295   300
Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp
305   310   315   320
Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro

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                325                 330                 335
Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Lys Leu
            340                 345                 350
Asn Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Ser
        355                 360                 365
Ile Val Tyr Tyr Asp Ser Asp Glu Leu Ile Phe Val Arg Asn Gly Asp
    370                 375                 380
Ser Lys Arg Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys
385                 390                 395                 400
Val Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His
                405                 410                 415
Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Tyr Val Glu Ser
            420                 425                 430
Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala Tyr Asp Pro Ala Ser Gly
        435                 440                 445
Gln Tyr Gly Tyr Thr Val Trp Ser Tyr Cys Gly Val Gly
    450                 455                 460
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<210> 314
<211> 460
<212> PRT
<213> Pyrococcus furiosus

<400> 314

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Val Asn Ile Lys Lys Leu Thr Pro Leu Leu Thr Leu Leu Leu Phe Phe
 1               5                  10                  15
Ile Val Leu Ala Ser Pro Val Ser Ala Ala Lys Tyr Leu Glu Leu Glu
            20                  25                  30
Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Gly Gly
        35                  40                  45
Gly Ile Trp Trp Asp His Ile Arg Ser Lys Ile Pro Glu Trp Tyr Glu
    50                  55                  60
Ala Gly Ile Ser Ala Ile Trp Leu Pro Pro Pro Ser Lys Gly Met Ser
65                  70                  75                  80
Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly
                85                  90                  95
Glu Tyr Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe Gly Ser Lys Glu
            100                 105                 110
Glu Leu Val Arg Leu Ile Gln Thr Ala His Ala Tyr Gly Ile Lys Val
        115                 120                 125
Ile Ala Asp Val Val Ile Asn His Arg Ala Gly Gly Asp Leu Glu Trp
    130                 135                 140
Asn Pro Phe Val Gly Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala
145                 150                 155                 160
Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu Leu
                165                 170                 175
His Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Cys His
            180                 185                 190
His Lys Glu Trp Asp Gln Tyr Trp Leu Trp Lys Ser Asn Glu Ser Tyr
        195                 200                 205
Ala Ala Tyr Leu Arg Ser Ile Gly Phe Asp Gly Trp Arg Phe Asp Tyr
    210                 215                 220
Val Lys Gly Tyr Gly Ala Trp Val Val Arg Asp Trp Leu Asn Trp Trp
225                 230                 235                 240
Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu
                245                 250                 255
Leu Ser Trp Ala Tyr Glu Ser Gly Ala Lys Val Phe Asp Phe Pro Leu
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            260                 265                 270
Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Asn Asn Ile Pro Ala Leu
        275                 280                 285
Val Tyr Ala Leu Gln Asn Gly Gln Thr Val Val Ser Arg Asp Pro Phe
    290                 295                 300
Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp Asn
305                 310                 315                 320
Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro Val
                325                 330                 335
Ile Phe Tyr Arg Asp Phe Glu Glu Trp Leu Asn Lys Asp Lys Leu Ile
            340                 345                 350
Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Thr Ile
        355                 360                 365
Val Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Val Arg Asn Gly Asp Ser
    370                 375                 380
Arg Arg Pro Gly Leu Ile Thr Tyr Ile Asn Leu Ser Pro Asn Trp Val
385                 390                 395                 400
Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His Glu
                405                 410                 415
Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Arg Val Asp Ser Ser
            420                 425                 430
Gly Trp Val Tyr Leu Glu Ala Pro Pro His Asp Pro Ala Asn Gly Tyr
        435                 440                 445
Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
    450                 455                 460

<210> 315
<211> 484
<212> PRT
<213> Thermococcus sp.

<400> 315
Ser Glu Ser Gln Cys Thr Ala Thr Cys Thr Trp Arg Val Val Tyr Met
 1               5                  10                  15
Ser Ala Lys Lys Leu Leu Ala Leu Leu Phe Val Leu Ala Val Leu Val
            20                  25                  30
Gly Val Ala Val Ile Pro Ala Arg Val Gly Ile Ala Pro Val Ser Ala
        35                  40                  45
Gly Ala Thr Ser Arg Pro Ser Leu Glu Glu Gly Gly Val Ile Met Gln
    50                  55                  60
Ala Phe Tyr Trp Asp Val Pro Ala Gly Gly Ile Trp Trp Asp Thr Ile
65                  70                  75                  80
Arg Ser Lys Ile Pro Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp
                85                  90                  95
Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Ala Tyr Ser Met Gly Tyr
            100                 105                 110
Asp Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr
        115                 120                 125
Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn
    130                 135                 140
Thr Ala His Ser Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn
145                 150                 155                 160
His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Thr Asn Ser Tyr
                165                 170                 175
Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn
            180                 185                 190
Tyr Leu Asp Phe His Pro Asn Glu Val Lys Cys Cys Asp Glu Gly Thr
```

```
        195                 200                 205
Phe Gly Gly Phe Pro Asp Ile Ala His Glu Lys Ser Trp Asp Gln Tyr
    210                 215                 220
Trp Leu Trp Ala Ser Gln Lys Ser Tyr Ala Ala Tyr Leu Arg Ser Ile
225                 230                 235                 240
Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp
                245                 250                 255
Val Val Lys Asp Trp Leu Lys Trp Trp Ala Leu Ala Val Gly Glu Tyr
            260                 265                 270
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
        275                 280                 285
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe
    290                 295                 300
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
305                 310                 315                 320
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
                325                 330                 335
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
            340                 345                 350
Leu Thr Tyr Glu Gly Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu
        355                 360                 365
Trp Leu Asn Lys Asp Arg Leu Lys Asn Leu Ile Trp Ile His Asn Asn
    370                 375                 380
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Asn Asp Glu Leu
385                 390                 395                 400
Ile Phe Val Arg Asn Gly Tyr Gly Asn Lys Pro Gly Leu Ile Thr Tyr
                405                 410                 415
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
            420                 425                 430
Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
        435                 440                 445
Val Asp Lys Tyr Val Gly Ser Asn Gly Trp Val Tyr Leu Glu Ala Pro
    450                 455                 460
Ala His Asp Pro Ala Lys Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
465                 470                 475                 480
Cys Gly Val Gly
```

<210> 316
<211> 457
<212> PRT
<213> Thermococcus hydrothermalis

<400> 316

```
Met Ala Arg Lys Val Leu Val Ala Leu Leu Val Phe Leu Val Val Leu
 1               5                  10                  15
Ser Val Ser Ala Val Pro Ala Lys Ala Glu Thr Leu Glu Asn Gly Gly
            20                  25                  30
Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Gly Gly Gly Ile Trp
        35                  40                  45
Trp Asp Thr Ile Ala Gln Lys Ile Pro Asp Trp Ala Ser Ala Gly Ile
    50                  55                  60
Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr
65                  70                  75                  80
Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Tyr
                85                  90                  95
Gln Lys Gly Ser Val Glu Thr Arg Phe Gly Ser Lys Glu Glu Leu Val
```

```
            100                 105                 110
Asn Met Ile Asn Thr Ala His Ala His Asn Met Lys Val Ile Ala Asp
        115                 120                 125
Ile Val Ile Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe
    130                 135                 140
Thr Asn Ser Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys
145                 150                 155                 160
Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly
                165                 170                 175
Asp Ser Gly Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser
            180                 185                 190
Trp Asp Gln His Trp Leu Trp Ala Ser Asn Glu Ser Tyr Ala Ala Tyr
        195                 200                 205
Leu Arg Ser Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly
    210                 215                 220
Tyr Ala Pro Trp Val Val Lys Asn Trp Leu Asn Arg Trp Gly Gly Trp
225                 230                 235                 240
Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Ser Trp
                245                 250                 255
Ala Tyr Asp Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys
            260                 265                 270
Met Asp Glu Ala Phe Asp Asn Asn Asn Ile Pro Ala Leu Val Asp Ala
        275                 280                 285
Leu Lys Asn Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val
    290                 295                 300
Thr Phe Val Ala Asn His Asp Thr Asn Ile Ile Trp Asn Lys Tyr Pro
305                 310                 315                 320
Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro Ala Ile Phe Tyr
                325                 330                 335
Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu Arg Asn Leu Ile
            340                 345                 350
Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Asp Ile Ile Tyr Tyr
        355                 360                 365
Asp Ser Asp Glu Leu Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro
    370                 375                 380
Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp
385                 390                 395                 400
Val Tyr Val Pro Lys Phe Ala Gly Ser Cys Ile His Glu Tyr Thr Gly
                405                 410                 415
Asn Leu Gly Gly Trp Ile Asp Lys Trp Val Asp Ser Ser Gly Arg Val
            420                 425                 430
Tyr Leu Glu Ala Pro Ala His Asp Pro Ala Asn Gly Gln Tyr Gly Tyr
        435                 440                 445
Ser Val Trp Ser Tyr Cys Gly Val Gly
    450                 455

<210> 317
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 317
Ser Ala Leu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val
 1               5                  10                  15
```

```
Pro Gly Gly Ile Trp Trp Asp Ile Lys Ile Pro Trp Ala Gly Ile Ser
            20                  25                  30
Ala Ile Trp Pro Pro Ser Lys Gly Met Gly Tyr Ser Met Gly Tyr Asp
        35                  40                  45
Pro Tyr Asp Phe Asp Leu Gly Glu Tyr Gln Lys Gly Glu Thr Arg Phe
    50                  55                  60
Gly Ser Lys Glu Leu Ile Thr Ala His Lys Val Ile Ala Asp Val Ile
65                  70                  75                  80
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Tyr Thr Trp
                85                  90                  95
Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu
            100                 105                 110
Asp Phe His Pro Asn Glu Asp Gly Thr Phe Gly Gly Pro Asp Ile His
        115                 120                 125
Lys Trp Asp Gln Trp Leu Trp Ser Ser Tyr Ala Ala Tyr Leu Arg Ser
    130                 135                 140
Ile Gly Asp Trp Arg Phe Asp Tyr Val Lys Gly Tyr Trp Val Val Trp
145                 150                 155                 160
Leu Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu
                165                 170                 175
Trp Ala Tyr Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys
            180                 185                 190
Met Asp Glu Ala Phe Asp Asn Asn Ile Pro Ala Leu Val Ala Leu Asn
        195                 200                 205
Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala
    210                 215                 220
Asn His Asp Thr Ile Ile Trp Asn Lys Tyr Ala Tyr Ala Phe Ile Leu
225                 230                 235                 240
Thr Tyr Glu Gly Gln Pro Ile Phe Tyr Arg Asp Glu Glu Trp Leu Asn
                245                 250                 255
Lys Asp Leu Asn Leu Ile Trp Ile His Leu Ala Gly Gly Ser Thr Ile
            260                 265                 270
Tyr Tyr Asp Asp Glu Ile Phe Val Arg Asn Gly Pro Gly Leu Ile Thr
        275                 280                 285
Tyr Ile Asn Leu Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Cys
    290                 295                 300
Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Asp Lys Val Ser Gly
305                 310                 315                 320
Val Tyr Glu Ala Pro Asp Pro Ala Gly Tyr Gly Tyr Val Trp Ser Tyr
                325                 330                 335
Cys Gly Val Gly
            340

<210> 318
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> clone

<400> 318
Met Arg Arg Ser Ala Arg Val Leu Val Leu Ile Ile Ala Phe Phe Leu
 1               5                  10                  15
Leu Ala Gly Ile Tyr Tyr Pro Ser Thr Ser Ala Ala Lys Tyr Ser Glu
            20                  25                  30
Leu Glu Gln Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro
```

```
        35                  40                  45
Glu Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln Lys Ile Pro Glu Trp
    50                  55                  60
Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly
65                  70                  75                  80
Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Tyr Phe Asp
                85                  90                  95
Leu Gly Glu Phe Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe Gly Ser
            100                 105                 110
Lys Glu Glu Leu Val Asn Met Ile Ser Thr Ala His Gln Tyr Gly Ile
        115                 120                 125
Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp Leu
    130                 135                 140
Glu Trp Asn Pro Tyr Val Gly Asp Tyr Thr Trp Thr Asp Phe Ser Lys
145                 150                 155                 160
Val Ala Ser Gly Lys Tyr Lys Ala His Tyr Met Asp Phe His Pro Asn
                165                 170                 175
Asn Tyr Ser Thr Ser Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile
            180                 185                 190
Asp His Leu Val Pro Phe Asn Gln Tyr Trp Leu Trp Ala Ser Asn Glu
        195                 200                 205
Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile Asp Ala Trp Arg Phe
    210                 215                 220
Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Ser
225                 230                 235                 240
Gln Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp
                245                 250                 255
Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe Asp Phe
            260                 265                 270
Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Lys Asn Ile Pro
        275                 280                 285
Ala Leu Val Tyr Ala Ile Gln Asn Gly Glu Thr Val Val Ser Arg Asp
    290                 295                 300
Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asn Ile Ile
305                 310                 315                 320
Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln
                325                 330                 335
Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Lys
            340                 345                 350
Leu Asn Asn Leu Ile Trp Ile His Glu His Leu Ala Gly Gly Ser Thr
        355                 360                 365
Lys Ile Leu Tyr Tyr Asp Asp Asp Glu Leu Ile Phe Met Arg Glu Gly
    370                 375                 380
Tyr Gly Asp Arg Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Asp
385                 390                 395                 400
Trp Ala Glu Arg Trp Val Asn Val Gly Ser Lys Phe Ala Gly Tyr Thr
                405                 410                 415
Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Arg Tyr Val
            420                 425                 430
Gln Tyr Asp Gly Trp Val Lys Leu Thr Ala Pro Pro His Asp Pro Ala
        435                 440                 445
Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr Ala Gly Val Gly
    450                 455                 460
```

<210> 319
<211> 306
<212> PRT

<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 319
Gly Gly Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Gly Gly Ile Trp
 1   5   10   15
Trp Asp Ile Lys Ile Pro Trp Ala Gly Ile Ser Ala Ile Trp Pro Pro
            20   25   30
Ser Lys Gly Met Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Asp
        35   40   45
Leu Gly Glu Gln Lys Gly Glu Thr Arg Phe Gly Ser Lys Glu Leu Ile
    50   55   60
Thr Ala His Lys Val Ile Ala Asp Val Ile Asn His Arg Ala Gly Gly
65   70   75   80
Leu Glu Trp Asn Pro Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser
                85   90   95
Gly Lys Tyr Ala Tyr Asp Phe His Pro Asn Asp Gly Thr Phe Gly Gly
            100   105   110
Pro Asp Ile His Gln Trp Leu Trp Ser Ser Tyr Ala Ala Tyr Leu Arg
        115   120   125
Ser Ile Gly Asp Trp Phe Asp Tyr Val Lys Gly Tyr Trp Val Val Trp
    130   135   140
Leu Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Trp
145   150   155   160
Ala Tyr Ser Ala Lys Val Phe Asp Phe Leu Tyr Tyr Lys Met Asp Ala
                165   170   175
Phe Asp Asn Asn Ile Pro Ala Leu Val Ala Gly Thr Val Val Ser Arg
            180   185   190
Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Ile Ile
        195   200   205
Trp Asn Lys Tyr Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro
    210   215   220
Ile Phe Tyr Arg Asp Glu Glu Trp Leu Asn Lys Asp Leu Asn Leu Ile
225   230   235   240
Trp Ile His Leu Ala Gly Gly Ser Thr Ile Tyr Tyr Asp Asp Glu Ile
                245   250   255
Phe Arg Gly Pro Gly Leu Ile Thr Tyr Ile Asn Leu Arg Trp Val Val
            260   265   270
Lys Phe Ala Gly Ile His Glu Tyr Thr Gly Leu Gly Gly Trp Asp Val
        275   280   285
Gly Val Ala Pro Asp Pro Ala Gly Tyr Gly Tyr Val Trp Ser Tyr Gly
    290   295   300
Val Gly
305

<210> 320
<211> 1392
<212> DNA
<213> Artificial Sequence

<220>
<223> clone

<400> 320
atgaggagat ccgcaagggt tttggttctg attatagcgt ttttcctcct ggcggggatt 60

tactacccct ccacgagtgc cgcgaagtac tccgagctgg agcagggcgg agtcataatg 120
caggccttct actgggacgt tccggaggga ggaatctggt gggacacaat acggcagaag 180
atccctgaat ggtacgatgc aggcatatcc gccatctgga tacccccggc gagcaagggc 240
atgggcgggg cctactcgat gggctacgac ccctacgatt acttcgatct gggcgagttt 300
taccagaagg gaaccgttga gacccgcttc ggctccaagg aagagctcgt caacatgatc 360
tccacggccc accagtacgg catcaaggtt atagcggaca tagtgataaa ccaccgcgca 420
ggtggagacc tcgaatggaa cccatacgtc ggcgactata cctggacgga cttttctaag 480
gtcgcctccg ggaaatacaa ggcccactac atggacttcc atccaaacaa ctacagcacc 540
tcagacgagg gaaccttcgg tggcttccca gacattgatc acctcgtgcc cttcaaccag 600
tactggctgt gggcgagcaa cgagagctac gccgcctacc tcaggagcat agggatcgat 660
gcgtggcgct ttgactacgt taagggctac ggcgcgtggg tcgtcaagga ctggctgagt 720
cagtggggcg gctgggccgt cggcgagtac tgggacacca acgtcgatgc gctcctcaac 780
tgggcctaca gcagcggcgc caaggtcttc gacttcccgc tctactacaa gatggacgag 840
gcctttgaca acaagaacat tcccgccctc gtttacgcca tccagaacgg tgaaaccgtc 900
gtcagcaggg atcccttcaa ggccgttacc ttcgtggcta accacgatac gaacataatc 960
tggaacaagt accctgccta tgccttcatc ctgacctacg aaggtcagcc cgtcatcttc 1020
taccgcgact acgaggagtg gctcaacaag gacaaactca acaacctcat atggattcac 1080
gagcacctgg caggggaag caccaagatc ctctactacg acgacgatga gctcatcttc 1140
atgagggaag gctacggcga caggcccggg cttataacct acatcaacct cggtagcgac 1200
tgggcggaga gatgggtgaa cgttggctca aagttcgcgg gctatacaat ccacgaatac 1260
accggaaacc tcggcggctg ggtcgacagg tacgtccagt acgacggctg ggtcaagctt 1320
accgctccgc cacacgatcc ggcaaacggc tattacggct actcggtctg gagctacgcc 1380
ggagttggat ga 1392

<210> 321
<211> 846
<212> DNA
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 321
ggcggtataa tgcaggcttc tatgggagtc cggaggaatt ggtgggacac ataagatccg 60
atgggcggat tcgcattgga tccccgcaga agggatggcg ggtatcatgg gctacgaccc 120
tacgatttga ctgggagtac agaagggatg aacgttggtc aaagacttaa atgatcacgc 180
caacataagg tatgcgaatg tataaccacc gcgcgggggc tgatggaacc tcctaacctg 240
gacgatttca agtgctcgga ataagccact actgacttcc accaacagag gacttggggt 300
ccgaatcacc taccagactg gcttgggcag cgaagctacg cgctactgga gcatggtgag 360
ctgggttgac tacgtaaggg ctagctgggt gtaactggct gtgggggggct gggcgtggga 420
gtactgggac acaacgtgag ctctactggg ctacagcggc aagtcttgac ttccctctac 480
tacaagatgg aggccttgaa aaaacatccg ctgtgctagg acgtgtccgg accttaagcg 540
tacttgtgca accacgaaca ataattggaa caagtacgct agcttcatcc tacctagagg 600
cagccatttt accgcgacta cgaggagtgg ctcaacaagg aataaacctc attggatcag 660
aacctgcggg gagacattta ctacgacgag atattttaga ggctaggcac cggctataac 720
taatcaacct gcggagtggg tagtcaagtt cgcggatcac gataacggac tcggggtggt 780
gacagtgttc gggggtatgc cccacgaccg caaggatagg ctactcgttg gagctacggg 840
tggtga 846